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02258 arabidopsis 09x187 arabidopsis 09unf arabidopsis 09na70 homo sapien 08ntr1 homo sapien 081808 arabidopsis 081808 arabidopsis 0810700 mus musculu 091m32 arabidopsis 073613 xenopus lae P70286 mus musculu 09ntr3 homo sapien 091y18 arabidopsis

065239 arabidopsis 042440 oryzias lat Q9zqn5 arabidopsis O43319 homo sapien Q9szm7 arabidopsis Q9pvw4 oryzias lat Q9ntr2 homo sapien

Searched:

Run on:

Database

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043317 homo sapien Q62073 mus musculu

Q9mae9 arabidopsis

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Inohara N., del Peso L., Koseki T., Chen S., Nunez G.;
"RICK, a novel protein kinase containing a caspase recruitment domain,
interacts with CLARP and regulates CD55-mediated apoptosis.";
J. Biol. Chem. 273:12296-12300(1998).
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Anome M., Hofmann K., Burns K., Martinon F., Bodmer J.-L.,
Mattmann C., Tschopp J.;
"Identification of CARDIAK, a RIP-like Kinase that associates with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-98307936; PubMed-9642260;
McCarthy J.V., Nl J., Dixit V.M.;
MRIP2 is a novel NF-kappaB-activating and cell death-inducing kinase.";
J. Biol. Chem. 273:16968-16975(1998).
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Platzer M., Varon R.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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Ozersky P., Holmes A., Broy M.;
Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
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01-JUN-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
SERINE/THREONINE KINASE RICK.
RICK OR RIP2.
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MEDLINE=98241596; PubMed=9575181;
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09stu7 arabidopsis
09m8c3 arabidopsis
09m8c3 arabidopsis
065833 lycopersico
05810 arabidopsis
082754 arabidopsis
091vq9 arabidopsis
09m8c2 arabidopsis
09m8c2 arabidopsis
09m8c2 arabidopsis
09m8c4 arabidopsis
09m8c6 arabidopsis
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Q9zsd8 lycopersico
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024027 lycopersico
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ETHYLENE.INDUCIBLE CTRI-LIKE PROTEIN KINASE.
Lycopersicon esculentum (Tomato).
Eukaryoparsicon esculentum (Tomato).
Magnoliophyta; endicotyledons; core endicots; Asteridae; euasterids I; Solanales; Solaname.
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                                                                                                                                                                                                                                                                                                                             8 SALPTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDVLREA 67
Pazdernik N.J., Donner D.B., Goebl M.G., Harrington M.A.;
"Mouse Interacting Protein 3 Does Not Contain a Caspase-Recruiting
a Death Domain but Induces Apoptosis and Activates NF-kappaB.";
MOI. Cell. Biol. 19:0-0(1999).
EMBL; AFI78953; ARF789313.1; -.
INTERPRO; IPR00179; -.
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PFAM; PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_ST; 1.
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462 TTASSSAKYDQAQFGRGRGW 481
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Best Local Similarity 28.09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVSQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLSTAGNSERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SKSAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPET
                                                                                                                                                                                                                                                                                                       ó.
                                                                                                                                                                                                                                                                         540;
                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                         575A692239505792 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                        Score 2823; DB 4;
Pred. No. 1.9e-220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ā
                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                              PFAM; PF00069; pkinase; 1.
PFAM; PF00619; CARD; 1.
PROSITE; PS00108; PF0TEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECEPTOR INTERACTING PROTEIN 3.
                                                                                                                                                                                                                            61194 MW;
    AAC24561.1; -AAC27722.1; -AAC25668.1; -AAC4634.1; -AAD04634.1; -AAD04634.1; -
                                                                                                                                                                                                                                                                         99.8%;
99.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                  HSSP; P00523; 2PTK.
INTERPRO; IPR000719; -.
INTERPRO; IPR001315; -.
INTERPRO; IPR002290; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wus musculus (Mouse)
                                                                                                                                                                                                                            540 AA;
                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 539; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                   AF064824;
AF117829;
                        AC004003
                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9QZLO
Q9QZLO;
                                                                                                                                                                                                               Kinase
                                                       EMBL;
                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421
                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                               61
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829 AA;
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                                         Kinase.
SEQUENCE
  PROSITE;
PROSITE;
PROSITE;
                                                                                             Query Match
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Eukaryota; Viridiplantue; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                             HR--KTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADF 165
                                                                                                                                                                                                                                                                                                                                                                                                                 --HIHTPLLDSERKDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLSKWRMMSLSQSRSSKSAPEGGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                            GEAICSALPT------IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHL- 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPH--RARMISLIESGWAQNPDERP
                                                                                                                                                                                                                                                                     49;
                                                                                                                                                                                                                                         DB 10; Length 806;
                    Ethylene-inducible tomato CTR1-like protein kinase.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AFI10519; AAD10057.1;
RHSZP; P06213; LIRK.
RIVERPRO; IPR001249; -...
RIVERPRO; IPR001249; -...
RIVERPRO; IPR001249; -...
RAM; PF00069; pkinase; 1.
RPRIVES; PS00109; FRVEIN_KINASE_ATP; 1.
RPROSITE; PS00109; PROTEIN_KINASE_ATP; 1.
RPROSITE; PS00110; PROTEIN_KINASE_ST; 1.
RPROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CO. ALLSA CRAIG;
A Kannan P., Giovannoni J.J.;
Kannan P., Giovannoni J.J.;
Rithylene-inducible tomato CTRI-like protein kinase.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
REMBL; ARI10518; AAD10056.1; -
HISSP; P06213; 11RK.
A HISSP; PR001245; -
A INTERPRO; IPR001245; -
A INTERPRO; IPR001245; -
A INTERPRO; IPR001245; -
A INTERPRO; IPR001245; -
A INTERPRO; PR00169; -
A INTERPRO; PR00169; -
A INTERPRO; PR00109; TYRKINASE.
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                   89387 MW; 9102529F49549A61 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
ETHYLENE INDUCIBLE CTR1-LIKE PROTEIN KINASE.
                                                                                                                                                                                                                                       Query Match 13.8%; Score 389.5; DB 10; Best Local Similarity 34.0%; Pred. No. 4.5e-23; Matches 107; Conservative 55; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       829 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           || : | |: SFSTIMDMLRPHLKS 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SFLKCLIELEPVLRT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                   806 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Solanales; Solan
NCBI_TaxID=4081;
                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                        Kinase
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Magnollophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
Solanales; Solanaceae; Solanum.
NCBL_TaxID=4081;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. EVITA; TISSUE-GREEN FRUIT;
Zegzouti H., Jones B., Frasse P., Marty C., Maitre B., Latche A.,
Pech J.C., Bouzayen M.;
"Ethylene-regulated gene expression in tomato fruit: characterization
                                                                                                                                                                                                                                                                                                                                                                                            669
                                                                                                                                                                                                                                                                                                                                                                                                                                                     HR--KTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADF 165
                                                                                                                                                                                                                                                                                                                                                                                                                                GLSKWRMMSLSQSRSSKSAPFGGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVL 223
                                                                                                                                                                                                                                                                              --HIHTPLLDSERKDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPH--RARMISLIESGWAQNPDERP 281
                                                                                                                                                                     Gaps
                                                                                                                                                                                                     3 GEAICSALPT-----IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHL- 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of novel ethylene-responsive and ripening-related genes isolated by differential display."; Plant all display."; Plant J. 18:589-600(1999).

EMBL, Y13273; CAA73722.1; ---
EMBL, AF096250; AAD46406.1; ---
HINTERPRO; IPR00219; ---
INTERPRO; IPR002290; ---
                                                                                                                                                                                                                                                                                                     EQDFHAERL----KEFLREVAIMKRLRHPNIVLFWGAVIQPPNLSIVTEYLSRGSLYRLL
                                                                                                                                                                                                                                                                                                                                                                            49;
                                                                                                                              Length 829;
                                                                                                                                                                     Indels
                                                                       91889 MW; 9E976BF7640CE11D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-07N-1998 (TrEMBLrel. 05, Created)
01-07N-1998 (TrEMBLrel. 05, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 91.9 KDA PROTEIN.
                                                                                                                          13.8%; Score 389.5; DB 10; 34.0%; Pred. No. 4.6e-23; Live 55; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         829 AA
PSO0107; PROTEIN_KINASE_ATP; 1. PSO0108; PROTEIN_KINASE_ST; 1. PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00069; pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang Y., Li N.;
Plant Physiol. 114:1135-1135(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lycopersicon esculentum (Tomato)
                                                                                                                                               Best Local Similarity 34.0
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 801 SFSTIMDMLRPHLKS 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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Gaps
HKARESYIFPILGICNEPEF ----LGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRIL 125
                                                                     HEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAP 185
                                                                                       186 EGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSV-SQ 244
                                                                                                                                                                                                               245 GHRPVINEESLPY---DIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEIT 301
                                                                                                                                                                                                                                  20 DLRYLSRGASGTVSSARHADWR-VQVAVKHLHIHTPLLDSERKDVLRE----AEILHKA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 108 0 KDA PROTEIN.
TY2A6.310 OR AT4634480.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Embryophyta; Tracheophyta; Spermatophyta;
Bukaryota; Autidiplantae, Embryophyta; Tracheophyta; Bukaryota, Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>.</u>
                                   65 ASLDNEFVLRLEGVIEKVNWDQDPKPALVTKFWENGSLSGLLQSQCPRP---WPLLCRLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Zimmentann W., Wambutt R., Kalicki J., Wohldmann Zimmenmann W., Grueneisen A., Wambutt R.F.X.; Smith A., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12.7%; Score 359.5; DB 10; Length 963; 31.7%; Pred. No. 1.5e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Bavan M., Zimmermann W., Grueneisen A., Wambutt R., Bancroft
Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing project;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107993 MW; 10DD8910F44C140E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              963 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00069; pkinase; 1.
PRINTS; PR00109; TYRINASE.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Hypothetical protein.
SEQUENCE 963 AA; 107993 MW; 10DD8910F
                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                    302 FLEAVIQLKKTKLQSVSSA 320
                                                                                                                                                                                                                                                                                                                      293 NMNAAVSTVKDFLSQLKSS 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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SEQUENCE FROM N.A.
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                                                                                                              12;
                                                                                                                                                                                                                                                                                                                                                             225
                                                                                                                                                                                                                                                                                                                                                                                  283
                                                                                                                                                                        641
                                                                                                                                                                                                                                                                                        HRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGL 167
                                                                                                                                                                                                                                                                                                                          701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                     50 --HIHTPLLDSERKDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELL 107
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11 PTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDVLREAEIL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GEAICSALPT------IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHL- 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDIINE-99272740; Pubmed-10339433;
Yu P.W., Huang B.C., Shen M., Quast J., Chan E., Xu X., Nolan G.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Payan D.G., Luo Y.; a RIP-11ke kinase that activates apoptosis "Identification of RIP3, a RIP-11ke kinase that activates apoptosis
                                                                                                                                                                                                                                           EQDFHAERL----KEFLREVAIMKRLRHPNIVLFWGAVIQPPNLSIVTEYLSRGSLYRLL
                                                                                                                                                                                                                                                                                                           SKWRMMSLSQSRSSKSAPEGGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVLSR
                                                                                                                                                                                                                                                                                                                                                                                                                                 226 KOPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPH--RARMISLIESGWAQNPDERPSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                              45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 13.3%; Score 375; DB 4; Length 518; Best Local Similarity 31.3%; Pred. No. 3.6e-22; Matches 100; Conservative 62; Mismatches 127; Indels
                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                       13.6%; Score 385.5; DB 10; Length 33.2%; Pred. No. 9.8e-23; .ive 56; Mismatches 108; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     518 AA; 56901 MW; 38A3ECFBEBBD4151 CRC64;
                      08FCF7468993537D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
     Hypothetical protein; Kinase.
SEQUENCE 829 AA; 91912 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURT. BIO1. 9:539-542(1999).
EMBL; AF156884; AAD39005.1;
HSSP; PO8631; 1AD5.
INTERRO; IPRO00719; -.
INTERPRO; IPRO01245; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-OCT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00109; TYRKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00069; pkinase; 1.
                                                                                                            Matches 104; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              803 STIMDMLRPHLKS 815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        284 LKCLIELEPVLRT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIP-LIKE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and NFkappaB.",
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                                                                            Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09Y572
                                                                                                                                                                                                                                                                                        108
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DPDARPEFKEISVMLTNLLR-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P---VNHGPQEESCGSSQLHEN 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94; Conservative
                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P08631; 1AD5.
INTERPRO; IPR000719; -.
INTERPRO; IPR001245; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                            NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                      Salanoubat M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229
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                                                                                                                                 846
EIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPENYE 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSRGASGTVSSARHADW-RVQVAVK---HLHIHTPLLDSERKDVLREAEILHKARFSYIF 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
Maitl R., Ronning C.M., Koo H., Fujil C.Y., Utterback T.R.,
Barnstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC FSE6 genomic sequence.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC020580; AAF63631.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKT--EYPDVAWPLRFRI----LH
                                                                                                                   | |:|||| : ||::| |||: |:|| HAAKGLNYLHCLNPPVVHWDLKSPNLLVDKNWTVKVCDFGLSRFKANTFIPSKSVAGTPE
                                                                                                                                                                           187 GGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --RNESADEKSDIYSFGVVLWELATEKIPWETL-NSMQVIGAVGFMDQRL----EIPKDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEITFLEAVIQLKKTK 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D--PRWISLAESCWHSDTKLRPIFQELMDKLRDLQRKY-----MIQFQAIR 761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36;
                                                                                                                                                                                                                    244 QGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 773;
                                                                                                                                                                                                                                     102; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C1B70D3E6848A340 CRC64;
                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 353; DB 10;
; Pred. No. 3.8e-20;
62; Mismatches 102;
                                                                                                                                                                                                                                                                                                                            773 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     773 AA; 86054 MW;
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32.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94; Conservative
                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinase.
SEQUENCE
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Q9M8C1; 09м8С1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 VAVKHLHHT--PLLDSERKDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  276 NPDERPSFLKCLIELEPVLRTFEEITFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNI 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----IGTTL 312
                                                                                                                                                                                                                Eukaryota, Viridipiantae, Embryophyta; Tracheophyta, Spermatophyta, Magnoliophyta; eudicotyledons, core eudicots, Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       102 SLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEF-HV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           216 AVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPHRARMISLIESGWAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 KIADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPENYEP-----GQKSRASIKHDIYSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
Mewes H.W., Mayer K.F.X., Lemcke K., Schueller C., Quetier F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                 Bloecker H., Mewes H.W., Lemcke K., Mayer K.F.X., Quetier Salanoubat M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EU Arabidopsis sequencing project;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
ERBL; AL13299; CABGA442.1; -.
EMBL; AL049862; CAB42902.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EU Arabidopsis sequencing project;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                370 AA; 42328 MW; A508F716B432804B CRC64;
03S7D5;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PROTEIN KINASE ATNI-LIKE PROTEIN
T3A5.110 OR F18B3.10.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---RMSSDSS---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.3%; Score 348.5; DB 1
29.2%; Pred. No. 3.2e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00069; PKinase; 1.
PRINTS; PR00109; TYRKINASE.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
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us-09-445-223-1.rspt

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AILSA CRAIG;
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NCBI_TaxID=3702;
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01-OCT-2000
                                                                                                                                                              SEQUENCE
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                                                                                                                                                   Kinase
                                                                                                                                                                                                                                                                                                                                                                                           864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80 PILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 PGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVINEE-SLPYD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259 IPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEITFLEAVIQLKKTKLQSVS 318
                                                                                                                                                                                                                                                                                                                                                                 24 LSRGASGTVSSARHADW-RVQVAVKHL---HIHTPLLDSERKDVLREAEILHKARFSYIF 79
                                                                                             Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Brasnoliophyta; endicoryledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                 STRAIN-CV. COLUMBIA;
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,
Bainstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thallana chromosome III BAC F5E6 genomic sequence.";
Submitted (ARR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                 505 LFMGAVTLPQGLCIVSEFLPRGSLFRLLQRNMSKLD--WRRRINMALDIARGMNYLHRCS
                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPENYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  45;
                                                                                                                                                                                                                                                                                                        12.3%; Score 348.5; DB 10; Length 763;
                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                         763 AA; 85593 MW; F6787110603C597C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
1-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PROTEIN KINASE, PUTATIVE.
                                                                                                                                                                                                                                                                                                                 ilarity 31.9%; Pred. No. 8.7e-20;
Conservative 57; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              981 AA
                               763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lycopersicon esculentum (Tomato).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07,
07,
15,
                                                                                                                                                                                                                                                   EMBL; AC020580; AAF63629.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    319 SAIHLCDKKK 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----LSDKNK 721
                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTR2 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1998
01-OCT-2000
                                                                                                                                                                                                                                                                                                                               66;
                                                                                                                                                                                                                                                                 Kinase.
SEQUENCE
                                                                                                                                                                                                                                                                                                       Query Match
Best Local Si
Matches 99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              065833
065833;
                                           09MBC3;
                               09M8C3
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065833
            RESULT
                      09M8C3
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67 AEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILH 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantee; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>`</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   804 DVAXGMDCLHTSNPTIVHRDLKSPNLLVDTDWNVKVCDFGLSRLKHNTFLSSKSTAGTPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHLHIHTPLLDSE-----RKDVLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 EIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 GGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic sequence.";
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STRAIN-CV. COLUMBIA:
Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu l
Lin X., Kaul S., Town C.D., Benito M., Creask T.R., Barnstead M.E.
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome I BAC F25P22 genomic sequence."
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
EBBL; ACO12679; AAF24836.1; --
HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244 QCHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             913 QNKRLEIPKELDPI-----VARIIWECWQTDPNLRPSFAQLTVALTPLQR 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.0%; Score 340; DB 10; Length 90 30.8%; Pred. No. 6e-19; ive 56; Mismatches 108; Indels
Lin Z., Hackett R.M., Payton S., Grierson D.;
Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ005077; CAA06334.1; --
HSSP; P12931; 1FMK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           04522B40F3425068 CRC64;
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1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
1-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                  INTERPRO, IPR002290; -.
PFAM; PF00069; pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS00449; ATPASE_A; UNKNOWN_L.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                     MENDEL, 29910; Lyces;2342;29910.
INTERPRO; IPR000568; -.
INTERPRO; IPR000719; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  981 AA; 107175 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL 112.2 KDA PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 12.0°
Best Local Similarity 30.8°
Matches 90; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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11;

E47D333311805B52 CRC64

82281 MW;

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736 AA;
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SEQUENCE 83
    SEQUENCE
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                                                                                                                                                                                                                                           10;
                                                                                                                                                                                                                                                                                                                                                                                EFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLK 148
                                                                                                                                                                                                                                                                                                                                                                                                      757 GSYGEVYRGDWHGTEVAVKKF-LDQDLTGEALEEFRSEVRIMKKLRHPNIVLFMGAVTRP 815
                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                       88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Peters S.A., van Staveren M., Dirkse W., Stiekema W., Bancroft I., Mewes H.W., Mayer K.F.X., Schueller C., Bevan M.; Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                     GTVSSARHADWR-VQVAVKHLHIHTPLLDSERKDVLREAEILHKARFSYIFPILGICNEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPH--RAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPE--NYEPGQKSRA
                                                                                                                                                                                              Length 1030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peters S.A., van Staveren M., Dirkse W., Stiekema W., Mewes
Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
PRINTS; PR00308; ANTIFREEZEI.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Hypothetical protein.
SEQUENCE 1030 AA; 112205 MW; 9BD7125FB1DF1B38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AL011018; CAA19821.1; -.
EMBL; AL161558; CAB79260.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       082754;
01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
PUTATIVE SERINE/THREONINE KINASE.
                                                                                                                                                                                       Query Match 11.9%; Score 337.5; DB 10; Best Local Similarity 34.8%; Pred. No. 1e-18; Matches 93; Conservative 39; Mismatches 108; 1
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PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PS00108; PROTEIN_KINASE_ST: 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              265 MISLIESGWAQNPDERPSFLKCLIELE 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00069; pkinase; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR000014; -. INTERPRO; IPR000719; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
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                                                                   Gaps
                                                                                                                    65 REAEILHKARFSYIFPILG-ICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPL--- 120
                                                                                                                                                                                                                    121 -RFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSR 179
                                                                                                                                                                                                                                                                  624
                                                                                                                                                                                                                                                                                                                   237
                                                                                                                                                                                                                                                                                                                                                                                                                   238 IMYSVSQGHRPVINEESLPYDIPH--RARMISLIESGWAQNPDERPSFLKCLIELEPVLR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         450 AGLPSHFHLQLSEIEFHEIIGSGSFGKVYKGRCRN--KIVAIKRYRANTYCSKSDVDMFC 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65 REAEILHKARFSYIFPILGIC-NEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 ILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 APEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8 SALPTIPYHKLADLRY---LSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDVL 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSKSAPEGGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQ
                                                                                                                                                                                                                                                                                                                                             Euteleostomi;
                                                                   35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wei Y.J., Ding J.F., Xiong H., Zhou Y., Hui R.T., Liew C.C.; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF116826; AAD29632.1; -.
                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutel.
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92850 MW; 3B21484B434F46E8 CRC64;
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Score 335.5; DB 10;
Pred. No. 9.3e-19;
.....neg 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 11.8%; Score 334.5; DB 4; Best Local Similarity 28.1%; Pred. No. 1.3e-18; Matches 116; Conservative 76; Mismatches 170;
  11 9%; Sco. 32.9%; Pred. No. 5... 32.9%; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPR00019; .
INTERPRO; IPR001145; .
INTERPRO; IPR002110; .
INTERPRO; IPR002110; ..
PFAM; PF00023; ank; 10.
PFAM; PF00109; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
PROSITE; PS001107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l protein.
835 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P00523; 2PTK.
                    Query Match
Best Local Similarity
Matches 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE-HEART;
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18;
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                                                                                         679 YHHIRPPIG-----YSIP--KPISSLLIRGWNACPEGRPEFSEVVMKLEECLCNIE---L 728
624 -- QPGNLRWMAPEVFT -- QCTRYTIKADVFSYALCLWEILTGEIPFAHL-KPAAAAADMA 678
                                                244 OGH-RPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEITF 302
                                                                                                                                           LEAVIQLKKTKLQSVSSAIHLCDKK------KMELSLNIPVNHGPQEESCG- 347
                                                                                                                                                                               62 DVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYP-DVAWPL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 KGFWIFEAGTYRWAAPELFSYDTLEIGEKKHYDHKVDVYSFAIVFWELLINKTPFKGKNN 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 RFRILHEIALGVNYLHNMTPPLLHHDLKTQNILL-DNEFHVKIADFGLSKWRMMSLSQSR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 SSKSAPEGGTIIYMPPENY----EPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTN 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       235 PLQIMYSVSQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             284 -IFVAYAASKNQRPSV--ENLPEGV-----VSILQSCWAENPDARPEFKEITYSLTNLL 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RTFEEITFLEAVIOLKKTKL---OSVSSAIH---LCD------KKKMELSLNIP 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |: | :| || :| || 335 RSLSSDT--DATSSNSKANIATEDSTSSLVQERVVCDCPGLKMSKTKKLKKKTNKLMNMI 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12 TIPYHKLADLRYLSRG---ASGTVSSARHADWR--VQVAVKHLHIHTP-----LLDSERK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
PROTEIN KINASE ATM1-LIKE PROPEIN.
Arabidopsis thaliana (Mouse-ear cress).
Bukasryota, Viridiplantae, Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61;
                                                                                                                                                                                                                                          348 -SSQLHENSGSPETSRSLP-APQDN-DFLSRKAQDCYFMKLHHCPGNHSWDST 397
                                                                                                                                                                                                                                                                                788 YSSQ---GLSLEEMKRSLQYTPIDKYGYVSDPMSSMHF---HSCRNSSSFEDS 834
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Best Local Similarity 30.1%; Pred. No. 7.1e-19;
Matches 112; Conservative 64; Mismatches 135; Indels 61;
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DNA Res. 7:31-63(2000).
EMBL; AB018119; BAA97277.1; -.
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SEQUENCE
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Title: Perfect score:

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Kinase of death (K
Arabidopsis CTR1 p
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Arabidopsis thalia
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Human Apop3 protei
Kinase of death (K
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Human Apop3 (K50D)
Human RIP-1 amino
Arabidopsis thalia
A human regulator
Barley EDR1. Hord
Tomato TCTR2. Lyc
Human CARK (Cardia
Novel protein kina
Skin cell protein,
Murine RIP protein
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Skin cell protein,
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Rice EDRI. Or...
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Human Apop3 (1-251
Eucalyptus grandis
                                                                 Mouse protein kina
                                                                                                                               Mouse receptor int
                                          Skin cell protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B1 protein; intracellular mediator; modulator; inflammation; cell death; cell survival pathway; intracellular signalling; AIDS; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                    B55946
W04627
W04627
W80994
W809994
B01526
B01526
W17938
W17938
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W17950
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B50439
B01470
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Y45047
B50440
Y45044
B25544
B56018
Y76123
B56062
Y79154
Y76007
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971L-0121011.
971L-0121199.
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Human B1 protein.
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05-JUN-1997;
30-JUN-1997;
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340.5
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W92795
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Amino acid sequenc
Human cancer assoc
Human RICK protein
Human RICK protein
Human RICK protein
Human RICK protein
Breast and ovarian
                                                                                                                                      June 14, 2001, 08:04:28; Search time 51.9 Seconds (without alignments) 594.762 Million cell updates/sec
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(SIDS6/gcgdata/geneseq/geneseqp/AA1980.DAT:*

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               GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                             390729 seqs, 57163235 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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Match Length
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999.8
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New B1 protein regulates cell death and cell survival pathways derivatives, DNA and antibodies, also regulate intracellular

Amino acid sequenc Murine protein kin

B58938 Y69163 Y76079

2823 2823 2817 2774 2497 1475 867 797 577

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Wallach

Boldin M, Malinin N, WPI; 1999-070258/06. N-PSDB; X02558. ~

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Baughn MR; .
H, Azimzai Y;
                  /note= "protein kinase family signature sequence"
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tone GA, Yue
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267
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296
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457.
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oung J, Gorgone GA,
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Bandman O, Au-Young J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "potential
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98US-0173482.
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99US-0173482.
99US-0229005.
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N-PSDB; Z46143.
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Reddy R, Lu DAM,
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12-JAN-1999;
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Patterson C,
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14-SEP-1998;
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19-NOV-1998;
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  Region
TIL TIL TELLE TELL
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                                                                         This invention describes the isolation of a novel human B1 protein which can interact with, intracellular mediators or modulators of inflammation, cell death and/or cell survival pathways, directly or indirectly. Cells can be modulated or mediated in inflammation, cell death or cell survival pathways or another intracellular signalling activity using B1. Conditions such as AIDS and cancer can be treated using B1. Antibodies, oligonucleotides and ribozymes can also be used to regulate the above
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                                                                                                                                                                                                                                                                                                                  Length 540;
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                                                                                                                                                                                                                                                                                                                  DB 20;
                                                                                                                                                                                                                                                                                                                100.0%; Score 2829; DB 20
100.0%; Pred. No. 5.2e-257
Live 0; Mismatches 0;
    cancer
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  inflammation; for treating AIDS,
                                        Claim 4; Fig 3A; 90pp; English.
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ID Y68774 standard; Protein; 540
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                                                                                                                                                                                                                                                           540 AA;
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Matches 540;
                                                                                                                                                                                                                                                           Sequence
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    treatment
                                                                Y68769-95 and Y68797-99 represent human phosphorylation effectors (PHSP designated PHSP1-PHSP31 (the protein Sequence for PHSP28 is not given in the specification). The sequences were isolated from cDNA ilbraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, fimmune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing disorders associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   300
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diagnosis; cytostatic; proliferative; vulnerary; immunomodulator;
antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                          KDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPL 120
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                prevention of proliferative, immune and neuronal disorders
human phosphorylation effectors useful for the diagnosis,
                                                                                                                                                                                                                                                                             Length 540;
                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                          1.9e-256;
                                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                                          Score 2823; DB
Pred. No. 1.9e-
0; Mismatches
                                                                                                                                                                                                   with increased PHSP expression/activity.
                                           Page 84-85; 142pp; English.
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                                                                                                                                                                                                                                                                        99.8%;
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                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                               540 AA;
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                                                                                                                                                                                                                                                                                       Best Local Sim
Matches 539;
                                           Claim 1;
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C77607 to C78448 encode the human cancer associated proteins given in 843398 to B44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: Cytostatic; proliferative, vulnerary; immunomodulator; antidiabetic; antisthmatic; antistlammatory; antiallammatory; antiallammatory; antiallammatory; antiallammatory; antithyroid; antiallargic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootroplic; antipsoriatic and antiangiogenic. The polynucleotides and polyneptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haemacopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in the exemplification of the present
                 dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasctropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acids comprising sequences encoding peptides
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antiinflammatory; antithyroid; antiallergic; antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 2823; DB 21;
Pred. No. 1.9e-256;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      useful for treating or diagnosing e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 1595-1597; 2352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.8%;
                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                           08-MAR-2000; 2000WO-US05882.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.8
Best Local Similarity 99.8
Matches 539; Conservative
                                                                                                                                                                                                                                                                                                                                                                         Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-587533/55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          544 AA;
                                                                                                                                                                                  WO200055350-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; C77779
                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                12-MAR-1999;
                                                                                                                                                                                                                      21-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                         Rosen CA,
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caspase recruitment domain; CARD-4; regulation; detection; caspase activation; detection; screening; therapy; diagnosis; disease; apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex; cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection; hormone-dependent tumour; autolimnume disorder; Alzheimer's disease; systemic lupus erythematosis; immune-mediated glomerulonephritis; stroke; Parkinson's disease; amyocrophic lateral sclerosis; retinitis pigmentosa; spinal muscular distrophy; cerebellar degeneration; anaemia; drug; myelodysplastic syndrome; mycoardial infarction; cell proliferation; cell differentiation; cell survival; CARD-41; CARD-45; CARD-41;
                                                                       360
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                                              304
                                                                                              364
                                                                                                                                           424
                                                                                                                                                                                                               185 sksapeggtiiymppenyepgqksrasikhdiysyavitwevlsrkgpfedvtnplqimy
                                                                                    SRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIIN
                                                                                                                                    PLSTAGNSERLQPGIAQQWIQSKREDIVNQWTEACLNQSLDALLSRDLIMKEDYELVSTK
                                    TFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPET
                       SVSQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel CARD-3 and CARD-4 genes and polypeptides used or treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "predicted kinase domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "predicted CARD domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "predicted linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                  Y31140 standard; Protein; 540 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0207359.
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98US-0099041.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .431
                                                                                                                                                                                                                                                                                                                                                                       Human CARD-3 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-494269/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARD-42; human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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17-JUN-1998
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This invention describes the isolation of moves in a proteins and a partial murine CARD-12 and CARD-4 polynucleotides and proteins of partial murine CARD-14 protein and genes. The genes and proteins of partial murine CARD-14 protein and genes. The genes and proteins of the invention are involved in the regulation of caspase activation.

The caspase recruitment domain (CARD) polynucleotides, polypeptides, homologues and antibodies can be used in screening assays, detection assays, predictive medicine and therapeutic and probpylactic methods of treatment. The methods may be used to diagnose and treat patients which are suffering from a disorder associated with abnormal level or rate of complex, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of the rank may be treated include cancer complex, abnormal activity of the caspase. Diseases that may be treated include cancer complex, and bormone-dependent tumours), autoimmune disorders (e.g. systemic lupus erythematosis, immune-mediated glomerulonephritis), viral in p53 and hormone-dependent tumours), autoimmune disorders (e.g. systemic lupus erythematosis, immune-mediated glomerulonephritis), viral infections, Alzheimer's disease, Parkinson's disease, amyotrophic lateral sclerosis, retinitis pigmentosa, spinal muscular dystrophy, cerebellar celegeneration, anaemia, myelodysplastic syndrome, myocardial infarction, and stroke. CARD-3 protein interacts with other cellular proteins, and so can be used for regulation of cellular proliferation and differentiation and cell survival. The CARD proteins may also be used to for screen drugs or compounds which modulate their activity. The CARD-4F gene can express a long transcript that encodes CARD-4F, and CARD-4Z. This sequence control of the human CARD-4 and CARD-4Z. This sequence represents the human CARD-3 protein described in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      540
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regulation of cellular proliferation and differentiation and cell
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                                                                                                      novel human
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Pred. No. 6.9e-256;
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                                                                                                      the isolation of
                                                            2; 181pp; English
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illarity 99.6%;
Conservative 0
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nes 538; Conserv
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                                                              Fig
                                                              Example 2;
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LPTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDVLREAEI

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This sequence is the human RICK (RIP-like interacting CLARP kinase)
protein of the invention. The RICK protein acts as a positive regulator
of apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10
during CD95 signalling. The invention provides methods for identifying
apoptosis signalling pathway inhibitors and activators, and methods and
compositions for screening compounds which will modulate the interactions
of the various compositions identified: ARC, RICK, and the CIDE family of
activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening
confositions for agents, useful in the diagnosis, prognosis or treatment of
disease associated with excess cell growth and dysregulation of
conpositions complexes containing RICK and CLARP can be used in drug
screening assays to identify inhibitor molecules blocking CD95-mediated
confositions of the enzymantic activity of caspase-8.
Confosition of ARC-like inhibitory compounds may be useful for gene
therapy treatment of disease with increased cell death in muscole tissue
and cardiac disorders. Therapeutic compositions of CIDEs can be used
confosition as reagents for the preparation or affinity chromatography
media, and for diagnostically measuring RICK levels: A specific inhibitor
confosition with intracellular factors such as cLARP and FADD appears to
confosition for appoptosis, inhibitors of RICK binding to intracellular
confosition as CLARP and FADD appears to
confosition for appoptosis, inhibitors of RICK binding to intracellular
confosition and for diagnostically decreased as reagents and protein as CLARP and FADD appears to
confosition for appoptosis, inhibitors of RICK binding to intracellular
confosition and for diagnostically decreased as reagents and protein as CLARP and FADD appears to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC;
481 ptrtskvrqlldttdiqgeefakvivqklkdnkqmglqpypeilvvsrspslnllgnksm 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Compositions for identifying apoptosis signalling pathway inhibitors useful for treating diseases -
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                                                                                                                                                                                          Y59404 standard; Protein; 531
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human RICK protein sequence.
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N-PSDB; 248762
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RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease.
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                                                                                                                                                                                                                                                               NDFLSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSE 429
                                                                                                                                                                                                                                                                           489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Compositions for identifying apoptosis signalling pathway inhibitors useful for treating diseases
                                                                                                                                     310 KKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQD
                                                                                                                                                                                                                               430 RLOPGIAOOWIOSKREDIVNOMTEACLNOSLDALLSRDLIMKEDYELVSTKPTRTSKVRQ
LHKARFSYIFFILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIA
                                                                            LGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGT
                                                                                                                       190 IIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPV
                                                                                                                                                                      INEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEITFLEAVIQL
                                                                                                                                                                                                                                                                                                                                                        490 LLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 540
                                                                                                                                                                                                                                                                                                                                                                     Human RICK protein sequence residues 54-531.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Koseki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Y59405 standard; Protein; 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-072163/06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         X59405;
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Gaps

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Score 2774; DB 21; Length 531; Pred. No. 7.4e-252; !; Mismatches 1; Indels 0;

1;

Best Local Similarity 99.6 Matches 529; Conservative

Similarity

Query Match

98.18; 99.68;

us-09-445-223-1.rag

Human RICK protein sequence residues 248-531.

21-MAR-2000 (first entry)

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This sequence is a fragment of the human RICK (RIP-like interacting CLARP Kinase) protein of the invention. RICK acts as a positive regulator of apoptosis, potentialing apoptosis induced by caspase-8 and caspase-10 during CD95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compositions identified: RCK, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening compositions identified: RCK, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening compositions identified: RCK is useful in screening compositions identified: RCK is useful in screening apoptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CD95-mediated apoptosis. Overexpression of ARC in an in vitro cell system can be used conformation of ARC-1 ke inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disease. AntiRICK antibodies can be used as reagents for the preparation or affinity chromatography median in the intracellular factors such as CLARP and FADD appears to be essential step in the blochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential factors are potential drug candidates.

Con be essential factors are potential drug candidates.

Con poptosis factors are potential drug candidates.

Con poptosis factors are potential drug candidates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 VLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 6.7e-226;
0; Mismatches 1;
Claim 6; Page -; 93pp; English.
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99.8%;
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Best Local Similarity 99.8'
Matches 477; Conservative
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                                                                                          61 rilheialgvnylhnmtppllhhdlktgnilldnefhvkiadfglskwrmmslsgsrssk 120
                                                                                                                               242
                                                                                                                                              slpapqdndflsrkaqdcyfmklhhcpgnhswdstisgsqraafcdhkttpcssalinpl 360
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                                                                                                                                                                                                                                                                                                                                                                 09
                                                                                                                                                                                                                                                                                                                                                                                                        483 RTSKVRQLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 540
                                     SAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSV
                                                                                                                                                                                    SQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEITF
                                                                                                                                                                                                LEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSR
                                                                                                                                                                                                                                                                                             SLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPL
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RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; cIDE-8; DREP-1; Atlagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease.
                                                                                                                                                                                               Compositions for identifying apoptosis signalling pathway inhibitors useful for treating diseases
                                                                                                                                                                                                                                                                                                                                                                                                     apoptosis factors are potential drug candidates.
Note: This sequence was created using information given in the
                                                                                                                                                                      Koseki T;
                                                                                                                                                                                                                      Claim 6; Page -; 93pp; English.
                                                                                                                             99WO-US09183.
                                                                                                                                           98US-0069023
                                                                                                                                                        (UNMI ) UNIV MICHIGAN
                                                                                                                                                                      Nunez G, Inohara N,
                                                                                                                                                                                    WPI; 2000-072163/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                    284 AA;
                                                                                                                              27-APR-1999;
                                                                                                                                           27-APR-1998;
                                                                                      Homo sapiens
                                                                                                   W09955134-A2
                                                                                                               04-NOV-1999.
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Gaps .; 0 Length 284; Indels Query Match 52.1%; Score 1475; DB 21; Best Local Similarity 100.0%; Pred. No. 3.1e-130; Matches 284; Conservative 0; Mismatches 0;

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257 YDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEITFLEAVIQLKKTKLQS 316

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421

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Y59406 ID Y59406 standard; Protein; 284 AA.

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This sequence is a fragment of the human RICK (RIP-like interacting CLARP Kinase) protein of the invention. RICK acts as a positive regulator of apoptosis, potentialing apoptosis induced by caspase-8 and caspase-10 during CD95 signalling. The invention provides methods for identifying apoptosis signalling pathway inhibitors and activators, and methods and compositions for screening compounds which will modulate the interactions of the various compositions identified: ACK, RICK, and the CIDE family of activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening assays for agents, useful in the diagnosis, prognosis or treatment of disease associated with excess cell growth and dysregulation of apoptosis. Complexes containing RICK and CLARP can be used in drug screening assays to identify inhibitor molecules blocking CD95-mediated apoptosis. Owexpression of ARC in an in vitro cell system can be used to identify inhibitors of the enzymatic activity of caspase-8.

C identification of ARC-like inhibitory compounds may be useful for gene therapy treatment of disease with increased cell death in muscle tissue and cardiac disorders. Therapeutic compositions of CIDEs can be used to treat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia, ischaemic injury, and toxin-induced liver disease. AntirRICK antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RICK; human; RIP-11ke interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-A; CIDE-B; DREP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemla; ischaemic injury; toxin-induced liver disease.
                                                                              436
                                                                                                                                                                            QQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDI 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Compositions for identifying apoptosis signalling pathway inhibitors useful for treating diseases -
                    AQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQPGIA
317 VSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRSLPAPQDNDFLSRK
                                                                                                                                                                                                                                     QGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSLNLLQNKSM 540
                                                                                                                                                                                                                                                   Human RICK protein sequence residues 365-531.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nunez G, Inohara N, Koseki T;
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                                                                                                                                                                                                                                                                                                                                                                   Y59407 standard; Protein; 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US09183
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can be used as reagents for the preparation or affinity chromatography media, and for diagnostically measuring RICK levels. A specific inhibitor of an essential step in the biochemistry of apoptosis is needed. RICK interaction with intracellular factors such as CLARP and FADD appears to be essential for apoptosis, inhibitors of RICK binding to intracellular apoptosis factors are potential drug candidates.

Note: This sequence was created using information given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral; antiallergic; hepatotropic; antidabetic; antinifammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder; Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thytoiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative collitis; cardiovascular disorder; wound healing; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular
                                                                                                                                                                                                                                                            374 SRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQP 433
                                                                                                                                                                                                                                                                                                                           493
                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                            434 GIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDT
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                                                                                                                                                                                               Length 167;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                      30.6%; Score 8b/; 25 100.0%; Pred. No. 1.8e-73; +ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                              Best Local Similarity 100.
Matches 167; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-611515/58.
                                                                                                                                                167 AA;
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                                                                                                              specification.
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breast and ovarian cancer. Included in the invention are sequences breast and ovarian cancer. Included in the invention are sequences (#22012 - #22014) which are used in the isolation are sequences characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; Immunosuppressive, nootropic; antidiabetic; antihiflammatory; antiulcer; ununerary; anticonvulsant; antidiabetic; antihiflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antihiflammatory antiulcer; vulnerary; anticonvulsant; antibacterial; and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune chyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatorid arthritis and ulcerarive colitis; cardiovascular disorders such as anyocardial ischaemias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and
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kinase; quality assurance agent; shelf life; marker.
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te= "this region contains a series of nine
tandem ankyrin repeats"
                                                                                                                                                                                                                                                                                                                                                              Length 153;
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                                                                                                                                                                                                                                                                                                                                                            Score 797; DB 21;
Pred. No. 5.9e-67;
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                          28.2%;
99.3%;
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98US-0099973.
99US-0119353.
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Matches 149; Conservative
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11-SEP-1998;
09-FEB-1999;
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                                                                                                                                                                                                                                                                                                                 Sequence
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The present sequence represents a murine death associated kinase protein, containing ankyrin repeats, designated DAKAR. The DAKAR polynucleotides containing ankyrin repeats, designated DAKAR. The DAKAR polynucleotides can be used to express the polypeptides, and as probes to identify mucleic acids encoding proteins having kinase activity. DAKAR polypeptides are used for purifying proteins, e.g. to measure protein activity, as quality assurance agents to monitor shelf life and stability of binding partner proteins; as research agents, e.g. in assays to determine protein kinase activity. To identify novel molecules involved in signal transduction pathways, and to identify therapeutic compounds which may interfere with a poptosis; as molecular weight and isoelectric focusing markers; as controls for peptide fragmentation; identification of unknown proteins, e.g. by comparison with proteins in databases; and for preparation of antibodies. The antibodies can be used in assays to detect the presence of the protein, and to purify the protein by immunoaffinity chromatography. The antibodies can also be used to block binding of the protein by and parkar binding partners. Compounds that inhibit or enhance the kinase activity of DAKAR can be used to treat diseases characterized by overproduction or upregulated production of DAKAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              385
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                                                                                                                                           Novel death associated kinase containing ankyrin repeats (DAKAR) used as molecular weight marker and as controls for peptide fragmentation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54 PLLDSERKDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEY 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MNGEA----ICSALPTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVK---HLHIHT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 IELEPVLRTFEEITFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | | | : : | | | esksearpessrlkrasappfdndcslsellsqldsglsqtlegpeelsrsssec---kl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 megegrgrwalgllrtfdagefagwekvgsggfgqvykvrhvhwktwlalkcspslhvd-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 PDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SLSQSRSSKSAPEG - - GTIIYMPPENYEPGQKSRA-SIKHDIYSYAVITWEVLSRKQPFE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    348 SSQLHENSGSPETSRSLPAPQDNDF------LSRKAQDCYFMKL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 577; DB 21; Length 786;
; Pred. No. 3.7e-45;
64; Mismatches 160; Indels 120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDA 462
                                                                                                                                                                                                           Claim 13; Page 10; 71pp; English.
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(IMMV ) IMMUNEX CORP.
                                                                                   WPI; 2000-195582/17
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                                           Virca
                                                                                                        N-PSDB; Z61161
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Best Local S
                                           Bird TA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and half follicle disorders. Sequences V75942-Y76123 represent polypeptides encoded by cDNA sequences Y75942-Y76121 represent polypeptides encoded by cDNA sequences Y75942-Y76121 represent polypeptides and half coll types. Sequences Y75942-Y76121, Y76020-Y76021, Y76019 are proteins with an N-terminal signal sequence, indicating that they are secreted. Sequences Y75986-Y75989, Y76061-Y76071, Y76106-Y76109 and Y76112-Y76122 are proteins with one or more putative transmembrane
                                                                                                                                                                                                                                                                                                                                                                        Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell; secreted; transmembrane; infilammation; cancer; neurological disease; angiogenesis; tumour vascularisation; growth disorder; developmental disorder; skin wound; hair follicle disorder; anti-inflammatory; cytostatic; neuroprotective; vulnery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Murison JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polynucleotides useful for the treatment of various conditions including wounds and cancer {\ }^{\circ}
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64; Mismatches 154; Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kumble A,
                                                                                                                                                                                                                                                                                                                         Murine protein kinase/ankyrin homologue, SEQ ID NO:334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
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120 dtsrl----mkilgpgdvdlvldssas1hlavea 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 195-196; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sleeman M, Watson JD,
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                                                                                                                                                      Y76079 standard; Protein; 787
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98US-0188930
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                                                                                                                                                                                                                                                                   27-MAR-2000
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                                                                                                       RESULT 11
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10 LPTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVK---HLHIHTPLLDSERKDVLRE 66

Conservative

169;

Matches

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Murison JG;
                                                                      244 QGHRPVINEESLPYDIPHR---ARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEI 300
                                                                                                                                                                                                                                                                 301 TFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPET 360
127 EIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPE 186
                                                                                                                                                                                                                                                                                                                                                                         322 krasappfdndcslsellsqldsgisqtlegpeelsrsssec---klpssssgkrlsgvs 378
                                                                                                                                                                                                                                                                                                                                                                                                                                            379 svdsafssrgslslsfereastgdlgptdigkklvdaii----sgdtsrl----mki 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases .
                                                                                                                        G--GTIIYMPPENYEPGQKSRA-SIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVS
                                                                                                                                             t-----setedlcekpdeevk---dlahepgeksslesksearpessrl
                                                                                                                                                                                                                                                                                                                                        SRSLPAPQDNDF-----HHCPGNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV; noctropic; neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kumble KD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sleeman M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 262-263; 352pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GENE-) GENESIS RES & DEV CORP LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-007495/01.
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keratinocyte growth and motility, inhibiting the growth of cancer cells, andulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukcocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Skin; dermal papilla; keratinocyte; neonatai foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell; secreted; transmembrane; inflammation; cancer; neurological disease; analyogenesis; tumour vaccularisation; growth disorder; developmental disorder; skin wound; hair follicle disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 G--GTIIYMPPENYEPGQKSRA-SIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVS 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGHRPVINEESLPYDIPHR -- - ARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPET 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         322 krasappfdndcs1se11sq1dsgisqt1egpee1srsssec---k1pssssgkr1sgvs 378
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                                                                                                                                                                                                                                                                                                                                                            AEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILH 126
                                                                                                                                                                                                                                                                                                                                                                                 EIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            svdsafssrgslslsfereastgdlgptdigkklvdaii----sgdtsrl----mki 428
                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                       10 LPTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVK---HLHIHTPLLDSERKDVLRE 66
                                                                                                                                                                                                                                                                                                                         1rtfdagefagwekvgsggfggvykvrhvhwktwlaikcspslhvd----drermellee 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kghrp----elppicrprpracasliglmgrcwhadpgvrp------tfgei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    t------setedlcekpdeevk---dlahepgeksslesksearpessrl
                                                                                                                                                                                                                                                     64; Mismatches 154; Indels 116;
                                                                                                                                                                                                                   Length 787;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 anti-inflammatory; cytostatic; neuroprotective; vulnery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine RIP protein kinase homologue, SEQ ID NO:409.
                                                                                                                             oligonucleotides for examining expression patterns.
                                                                                                                                                                                                                  Score 576; DB 22;
Pred. No. 4.6e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                440 IQSKREDIVNQMTEACLNQSLDA 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y76123 standard; Protein; 590 AA
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                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                      Similarity
                                                                                                                                                               787 AA;
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                                                                                                                                                                                                                                                       Matches 169;
                                                                                                                                                                 Sequence
                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238
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322 krasappfdndcslsellsqldsgisqtlegpeelsrsssec---klpssssgkrlsgvs 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QGHRPVINEESLPYDIPHR---ARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEI 300
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                              10 LPTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVK---HLHIHTPLLDSERKDVLRE 66
                                                                                                                                  Novel polynucleotides useful for the treatment of various conditions including wounds and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LSRKAQDCYFMKL-----HHCPGNH
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                                                                                                                                                                                                                                                                                                                                                                          Length 590;
                                                                                       Kumble A,
                                                                                                                                                                                                                                                                                                                                                                           20.3%; Score 574; DB 21; 33.4%; Pred. No. 4.5e-45; ive 65; Mismatches 154;
                                                                                       a,
                                                                                        Onrust
                                                                                                                                                               Claim 4; Page 231-232; 235pp; English.
                                                                                       Watson JD,
                                                                      GENE-) GENESIS RES & DEV CORP LTD.
                                           98US-0069726.
                          99WO-NZ00051
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                                                                                        Sleeman
                                                                                                          WPI; 2000-072177/06
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                                                                                                                                                                                                                                                                                                                                                  590 AA;
                                                                                                                    N-PSDB; Z61830.
                          29-APR-1999;
                                            29-APR-1998;
                                                     09-NOV-1998;
                                                                                        Strachan L,
       04-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                             168;
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EIALGVNYLHNMTPPLLHHDLKTONILLDNEFHVKIADFGLSKWRMMSLSOSRSSKSAPF 186
                            etavgmnflhcmsppllhldlkpanilldahyhvkisdfglakcngmshshdlsm----d 180
                                                                                                                                                                                                                                                                           TFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPET 360
                                                                                                                                                                                                                                                                                                                                                                                           393 SWDSTIS--GSQRAAF------CDHKTTPCSSAIINPLSTAGNSERLQPGIAQQW 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | || | || :| :| :| :| 379 svdsafssrgslslsfereastgdlgptdigkkklvdaii-----sqdtsrl-----mki 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of murine Fel, a novel protein kinase. The sequence represents translation (reading frame 3) of Genesis clone 971025TRAMON480HT (see 258584). The invention relates to purified murine polypeptides having kinase function (see Y79152-56) and isolated nucleic acids encoding them (see Z58582-86). Claimed vectors comparising the novel nucleic acids, and claimed host cells (bacterial, yeast, plant, insect or animal) transfected or transduced with the vectors, are used to produce the polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel murine polynucleotides encoding kinase polypeptides, used as probes to identify nucleic acids encoding proteins having kinase
                                                                                            G--GTIIYMPPENYEPGQKSRA-SIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVS
                                                                                                                      --setedlcekpdeevk---dlahepgeksslesksearpessrl
                                                                                                                                                                                      QGHRPVINEESLPYDIPHR---ARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEI
                                                                                                                                                                                                                                                                                                                                                                   -----HHCPGNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Y79154 standard; Protein; 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-US17577
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98US-0099973
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11-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Murison JG;
  ----CDHKTTPCSSAIINPLSTAGNSERLQPGIAQQW 439
                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                      nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 309-310; 352pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENESIS RES & DEV CORP LTD.
                                                                                                                                                                                                                                                                                                                                                                                    Skin cell protein, SEQ ID NO: 409.
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                                                                                                                                    451
                                                                                                                                                                                                                                                 B56062 standard; Protein; 590
                                                                                     440 IQSKREDIVNOMTEACLNOSLDA
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Matches 168;
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                                                                                                                                                                                                                                                                                                                                                                                                                       The kinase polypeptides and their fragments are used as mol. wt. and isoelectric focusing markers, and as controls for peptide fragmentation. They also have a number of therapeutic uses, as kinases play a central role in cellular signal transduction. As such, alterations in kinase expression and/or activation can have a profloud effect on a plethora of cellular processes, e.g. proliferation and programmed cell death (apoptosis). The kinase polypeptides could also be used to identify binding partner proteins, or as reagents to identify proteins that regulate or interact with them. They may also be used for preparation of antibodies useful for detection, purification, and for blocking binding of kinase polypeptides to their binding partners.
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US-08-483-322-1
US-08-478-882-1
US-08-451-405A-2
US-08-496-841C-137
                  US-09-296-715-25
US-07-920-281C-1
US-08-466-27-1
US-08-487-826B-13
US-09-247-373B-33
US-09-247-373B-33
US-08-330-108-1
US-08-32-10087-1
US-08-101-593-1
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compartible
COMPUTER: STEM: Windows 95
SOFTWARE: FastEBQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/019,942
            -09-247-373B-25
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Pred. No. 0;
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Patent No. 6033855
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NAME: Meiklejohn, Ph.D., An.
REGISTRATION NUMBER: 35,283
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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99.8%;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1931 base pairs
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US-08 -261-432-1
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        GenCore version
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TITGAGAACATTTGAAGAGATAACTTTTCTTGAAGCTGTTATTCAGCTAAAGAAAACAAA 1151
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Patent No. 5817479
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig G.
TITLE OF INVENTION: NOVEL HUMAN KINASE HOW
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3174 PORTER DRIVE CITY: PALO ALTO STATE: CA COUNTRY CALOURING
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US-08-700-575-31
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Patent No. 5367065

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Constitutive Triple Response Gene and TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and ADDRESSEE: No. 5367065ris
STREET: One Liberty Place - 46th Floor
                     Length 3516;
                                                     Indels
                   DB 4;
                                                     0; Mismatches 316;
                                      3.4e-14;
                     Score 102.4;
                                      Pred. No.
                   4.9%;
                                    Best Local Similarity 51.83
Matches 372; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19103
COMPUTER READABLE FORM:
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CITY: Philadelphia
STATE: PA
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                     Query Match
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Sequence 277, Application US/09188930A

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Ornust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011.c1
CURRENT APPLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match 10.0%; Score 210; DB 1; 1 Best Local Similarity 100.0%; Pred. No. 4.4e-39; Matches 210; Conservative 0; Mismatches 0;
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                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J
REGISTRATION NUMBER: 36749
REFERENCE/DOCKET NUMBER: SP-100 US
TELEPHONE: 415-855-0555
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
IMMEDIATE SOURCE:
LIBRARY: THP-1 Phorbol LPS
US-08-700-575-31
                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                       LENGTH: 210 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                     linear
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Best Local Similarity
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                                                                                                                           FILING DATE:
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LENGTH: 3516
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1988 TGACAGAATATTTGTCAAGAGGTAGTTTATACAGACTTTTGCATAAAAGTGGAGCAAGGG 2047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1808 CTGTCCACCGTGCTGAGTGGCATGGCTCGGATGTTGCTGTGAAAATTCTCATGGAGCAAG 1867
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Exter, Joseph R.
TITLE OF INVENTION: Constitutive Triple Response Gene and
TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2168 TIGACAAAAATATACAGTCAAGGTTTGTGATTTTGTGTCTCTC 2210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 81.4; DB 1; Pred. No. 1.8e-09; 0; Mismatches 201;
                                    SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            One Liberty Place - 46th Floor
                 COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/928,464 FILING DATE: 19920810
                                                                                                                                                                     ATTORNELL FOLLS.

NAME: Miller, Suzanne E.

REGISTRATION NUMBER: 32,279

REFERENCE/DOCKET NUMBER: UPN-1

TELECOMMUTCATION INFORMATION:

TELEPHONE: 215-568-3100

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2890 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.9%;
                                                                                                                                           CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 50.17
Matches 202; Conservative
                                                                                                                                                                                                                                                                                                                                LENGTH: 2890 base pai
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; NAME/KEY: CDS
; LOCATION: 118..2583
US-07-928-464-1
                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                         CLASSIFICATION:
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PCT-US93-07347-1
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1988 TGACAGAATATTTGTCAAGAGGTAGTTTATACAGACTTTTGCATAAAAGTGGAGCAAGGG 2047
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1808 CIGICCACCGIGCIGAGIGGCAIGGCICGGAIGTIGCIGIGAAAAIICICAIGGAGCAAG 1867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         660 acctgcacaatatgactcctctttacttcatcatgacttgaagactcagaatatcttat 719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               480 gatttagttacatttttccaattttgggaatttgcaatgagcctgaattttgggaatag
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APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TILLE OF INVENTION: CONSTITUTE OF TRIPLE OF TRIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2168 TIGACAAAAAATATACAGTCAAGGTTTGTGATTTTGGTCTCTC 2210
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                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 3.9%; Score 81.4; DB 5; Best Local Similarity 50.1%; Pred. No. 1.8e-09; Matches 202; Conservative 0; Mismatches 201;
                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             %2-08-003 311B-1; Sequence 1, Application US/08003311B; Patent No. 5444166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN-
TELECOMMUNICATION INFORMATION:
TELECHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2890 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19930805
                                                                                                                     COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                           19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION:
PCT-US93-07347-1
COUNTRY:
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TITLE OF INVENTION: and Mutations

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1808 CTGTCCACCGTGCTGAGTGGCATGGCTCGGATGTTGCTGAAAATTCTCATGGAGCAAG 1867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCCACCCTAACATTGTTCTCTTCATGGGTGCGGTCACTCAACCTCCAAATTTGTCAATAG 1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540 ttactgaatacatgccaaatggatcattaaatgaactcctacataggaaaactgaatatc 599
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.9%; Score 81.4; DB 1; Length 3:50.1%; Pred. No. 1.9e-09; tive 0; Mismatches 201; Indels
                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
TITLE OF INVENTION:
                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 5601322ris
STRRET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,432
FILING DATE: June 17, 1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/003,311
FILING DATE: January 12, 1993
ATTORNEY/AGENT INFORMATION:
NAME: LOAI Y. Beardell
REGISTRATION NUMBER: 34,293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UPN-1864
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                                                                     Sequence 1, Application US/08261432
Patent No. 5602322
                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
2IP: 19103
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: UP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEPAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 50.1
Matches 202; Conservative
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118..2583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                    STATE: PA
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; LOCATION:
US-08-261-432-1
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                                      ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and ADDRESSEE: No. 544166ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tggacaatgaatttcatgttaagattgcagattttggtttatc 762
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                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/003,311B
FILING DATE: January 12, 1993
CLASSIFICATION B00
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/928,464
FILING DATE: August 10, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UPN-1108
                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATJUANEL LOCAT Y. Beardell
REGISTRATION NUMBER: 34,293
REFREENCE/DOCKET NUMBER: UPN-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3033 base pairs
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Best Local Similarity 50.1%;
Matches 202; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; NAME/KEY: CDS
; LOCATION: 118..2583
US-08-003-3118-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
                                                                                                                                                         COUNTRY: U.S.A. ZIP: 19103
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                                                                                                                                                                                                                                                                                                                                                                                                    cagaatatcttattggacaatgaatttcatgt---taagattgcagattttggtttatca 763
                                                                                                                       764 aagtggcgcatgatgtccctctcacagtcacgaagtagcaaatctgcaccagaaggaggg 823
                                                                                                                                                 824 acaattatttatatgccacctgaaaactatgaacctggacaaaaatcaagggccagtatc 883
                                                                                                                                                                                                                                                                                                                                    613 aaacatgatgtatacagcttcgccattgtgatctggggtgtgcttacacagaataatcca 672
382 gtgggcatgaacttcctgcattgcatgtctccgccactgctgcacctagacctgaagcca 441
                                                                               442 gcgaacatcttgctggatgcccactaccaaatgtcaagatttcttgactttgggctggcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Procedures and Materials for TITLE OF INVENTION: Disease Resistance in Plants NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS: ADDRESSEE: Gownsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                023070-058940US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/567,375 FILING DATE: 04-DEC-1995 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 24, Application US/08587680A Patent No. 5977434
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C. APPLICANT: Wang, Guo-Llang
APPLICANT: Song, Wen-Yuang
APPLICANT: Scabo, Veronique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34,774
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (415) 576-0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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  660 acctgcacaatatgactcctcctttacttcatgacttgaagactcagaatatcttat 719
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                                                                                                                                                                                                                                                                                        Sequence 66, Application US/09188930A

Patent No. 6150502

GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Orrust, Rene
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: Compositions Isolated From Skin Cells
FILE REFERENCE: 11000.1011c1
CURRENT FALLICATION NUMBER: US/09/188,930A

CURRENT FILING DATE: 1998-11-09
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Pred. No. 8.1e-09;
0; Mismatches 323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local Similarity 50.6%;
Matches 365; Conservative
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LOCATION: (1690)
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US-09-188-930-66
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Pred. No. 0.00029;
4; Mismatches 159; Indels
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APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REPERENCE: PHM. 70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FRALESEQ for Windows Version 3.0
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Pred. No. 0.0021;
0; Mismatches 83;
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                          REFERENCE/DOCKET NUMBER: 40
TELECOMUNINCATION INFORMATION
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
         30628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 2.8%;
Best Local Similarity 48.1%;
Matches 151; Conservative
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Best Local Similarity 55.6%;
Matches 104; Conservative
                                                                                                                                                                             LENGTH: 1558 base pairs
TYPE: nucleic acid
GTRANDEDNESS: single
                                                                                                                 TELEX: 200291
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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       REGISTRATION NUMBER:
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TYPE: DNA
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA HYPOTHETICAL: NO ANTI-COLOR
                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO FRAGMENT TYPE: CORIGINAL SOURCE: US-08-455-550-7
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APPLICANT: MIRAKAMI, KAZUO
APPLICANT: UENO, NAOTO
APPLICANT: KATO, VUKIO
APPLICANT: KATO, VUKIO
TITLE OF INVENTION: XENOPUS LAEVIS BONE MORPHOGENETIC PROTEINS AND USE THE
                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           575 ctcctacataggaaaactgaatatcctgatgttgcttggcattgagatttcgcatcctg 634
                                                                                                                                                                                                                                                                                                                                                                                                                                             515 aatgagcctgaatttttgggaatagttactgaatacatgccaaatggatcattaaatgaa 574
                                                                                                                                                                                                                                                                                                                                                      455 gaagetgaaattttacacaaagetagatttagttacatttttccaattttgggaatttgc 514
                                                                                                                                                                                                                                                                                                                                                                                               835 GAACTTAACACATTAGGGAAGATCAGGCATAGGTACATTGTGAGACTGCTCGCGTTTTGT 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             895 TCAAACAAGGAAGTCAACTTGCTAGTTTATGAGTACATGCTAAATGGAAGCTTAGGTGAA 954
                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                             Length 1554;
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                                                                                                                                                                                                                                                        Score 61.8; DB 2;
Pred. No. 3.9e-05;
0; Mismatches 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dike, Bronstein, Roberts & Cushman STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette
COMPUTER: ITAM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455,550
FILING DATE: 31-MAY-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/056,564
FILING DATE: 30-APR-1993
APPLICATION NUMBER: 07/577,892
FILING DATE: 05-SEP-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 7, Application US/08455550
; Patent No. 5670338
                                                                                                                                       TOPOLOGY: linear

MOLECULE TYPE: cDNA (partial)

US-08-587-680A-24
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 base pairs
                                                                                                                                                                                                                                                        Query Match 2.99
Best Local Similarity 49.89
Matches 156; Conservative
                                                                                                            STRANDEDNESS: single
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MEDIUM TYPE: Diskette
COMPUTER: IBM Compat:
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ADDRESSEE: Dike, Bro
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                                                                                           nucleic acid
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STATE: M
COUNTRY:
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                                                                                                                                      729 aattteatgittaagattgeagattitggittateaaagiggegeatgatgicecteteae 788
                                                                                                                                                             609 cttggccattgagatttcgcatcctgcatgaaattgcccttggtgtaaattacctgcaca 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               565 accagaacccggtgctcctgcaccgggacctcaagccatccaacgtcctgctggacccag 624
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                                                                                                 398 accagaacccggtgctcctgcaccgggacctcaagccatccaacgtcctgctggacccag
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APPLICANT: MUNICH, ARNOLD
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 2.6%; Score 54.2; DB 3; Length 1873; Best Local Similarity 55.6%; Pred. No. 0.0022; Matches 104; Conservative 0; Mismatches 83; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, STREET: PO BOX 747 CITY: FALLS CHURCH
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ZENECA LIMITED
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
TITLE PRERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5-08-545-196B-10
Sequence 10, 608pplication US/08545196B
Patent No. 6080597
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09329418
Patent No. 6096539
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA; ORGANISM: Homo Sapiens
US-09-329-418-1
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1970 attaaagcttwawwraargktctttsrktaaatattagtctccctccatgacactgcagt 2029
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STREET: PO BOX 747
CTTY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PLANE: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: MELKI, JUDITH
APPLICANT: MUNICH, ARNOLD
TITLE OF INVENTION: SURVIYAL MOTOR NEURON (SMN)
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY
TITLE OF OFFICES: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 53.6; DB 3;
Pred. No. 0.0029;
6; Mismatches 120;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/545,196B
                                                                                                  J9-OCT-1995
                                                                                                                                                                                                                                  2121-110P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 12, Application US/08545196B
; Patent No. 6080577
                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: FARACI, C. J.
REGISCRATION NUMBER: 32,350
REFERENCE/DOCKET NUMBER: 2121-
TELECOMMUNICATION INFORMATION:
TELEFRAM: (703) 205-8000
TELEFRAM: (703) 205-8000
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1552 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 2.6
Best Local Similarity 49.2
Matches 122; Conservative
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                                                                                                                                                     CLASSIFICATION:
                                                                                                                                     FILING DATE:
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US-08-545-196B-12
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PCT/AU90/00530

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REFERENCE/DOCKET NUMBER: TRICE-0002 TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100 TELEPAX: 215-568-3439
                                                                     NAME: Feeney, Joanne Longo
REGISTRATION NUMBER: 35,134
                                       FILING DATE: 02-NOV-1989 ATTORNEY/AGENT INFORMATION:
   APPLICATION NUMBER: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                          TOPOLOGY: 1;
MOLECULE TYPE:
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FEATURE:
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FEATURE:
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; LOCATION:
US-07-867-106-2
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STREET: One Liberty Place 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                  Length 1582;
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APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 53895;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  Score 53.6; DB 3;
Pred. No. 0.0029;
                                                                                                                                                                                                                                                                                                                                                                                                                     6; Mismatches 120;
                                                                                      NAME: FARACI, C. J.
REGISTRATION NUMBER: 32,350
REFRENCE/DOCKET NUMBER: 2121-110P
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8000
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/07/867,106
FILING DATE: 19920625
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 5389526
                                                                                                                                                                                                                                                                                                                                                                                  2.6%;
                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                     LENGTH: 1582 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 49.2
Matches 122; Conservative
   CURRENT APPLICATION DATA:
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5837 AAAGTAACAATAGTACTAATAAAGATCTTTTAAATTTAATAATATACATTTTTAATGGTT 5778
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Pred. No. 0.006;
5; Mismatches 118; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: June 13, 2001, 17:33:58 Job time: 6861 sec
                                                                                                                                                      DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                              2.5%;
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                             LENGTH: 5852 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.55
Best Local Similarity 49.65
Matches 121; Conservative
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em_esthum20: em_esthum21:

em_esthum22:*
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em_esthum25:*
em_esthum27:*
em_esthum27:*

em_estin1:*
em_estin2:*
em_estin3:*
em_estin4:*

em_estov1:'
em_estov2:'
em_estpl1:'

em_estpl3: em_estpl4: em_estpl5:

em_estpl2

em_estin5: em_estom1: em_estom2:

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em_estrol6:*
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102
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9530.371 Million cell updates/sec
                                                                                                                    June 13, 2001, 11:10:10 ; Search time 1923.15 Seconds
                                                                                                                                                                                                                                   19247034
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                         9623517 seqs, 4368049070 residues
                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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em_esthum8:
em_esthum9:
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em_esthum2:
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gb_est40:*
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gb_est14::
gb_est15::
gb_est16::
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gb_est17::
gb_est18:;
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gb_est11:
gb_est12:
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gb_est22:
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gb_est37:
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9b_est2: *
9b_est4: *
9b_est6: *
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9b_est7: *
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Perfect score:
Sequence:
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                                                                      Run on:
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em_estpl9:*
em_estpl10:'
em_estrol:*
em_estro2:*

em_estp17: em_estp18:

em_estpl6

em_estrol3:* em_estrol4:* em_estrol5:*

em_estrol0:* em_estrol1:* em_estrol2:*

em_estro7: em_estro8: em_estro9:

em_estro4: em_estro6

em_estro3

em_estro20:

gb_est25: gb_est26: gb_est27: gb_est28: gb_est29: gb_est30: gb_est31:

gb_est32: gb_est41: gb_est42:

gb_est43: gb_est44: gb_est45: gb_est46: gb_est47:

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gb_est97:*
gb_est98:*
em_gss_fun:*
em_gss_hum1:*
em_gss_hum2:*
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em_gss_inv3:*
em_gss_other:*
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gb_est100:*

gb_est101:*

gb_est101:*

gb_est103:*

gb_est104:*

gb_est106:*

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gb_est101:*

gb_est101:*
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em_gss_invl
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9b_est48:*
9b_est49:*
9b_est49:*
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9b_est56:*
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9b_est66:*
9b_est66:*
9b_est66:*
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9b_est180; **
9b_est81; **
9b_est81; **
9b_est83; **
9b_est83; **
9b_est88; **
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	BG170405 602322736	BE877822 601486392	BE875947 601486423	BE551615 7a42g06.x	AW150819 xg39f08.x	AI745575 wc34f12.x	AW085560 wy67c04.x	AW960501 EST372572	BE536247 601062632	AI801150 to85h04.x	AA160647 zq49c11.r	BF125028 601762610	BF125423 601763549	AI307810 tb28d07.x	AI904799 IL-BT067-	AA161113 zo58d05.s	BE274455 601120495	AW593657 x194d07.x	
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Score	745.8	989	655.8	621.8	609.4	592	590.6	588.8	587	561	558.6	554	550.4	546.8	542	532.6	513.4	206	
Result No.		7	e	4	ທ	9	C 7	8	6	c 10	11	12	13	14	15	16	17	c 18	

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Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota: Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

Eukaryota: Dutheria: Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 828)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

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Tona i: Robert Strausberg@aih.gov

Tona i: Robert Strayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Righ quality Sequence stop: 795.
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/note="Corgan: lung: Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
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                                                                                           540 TACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACTGACATCCAAGG 599
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1 (bases 1 to 870)

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

4 National Institutes of Health, Mammalian Gene Collection (MGC)

5 Ontact: Robert Strausberg, Ph.D.

6 Contact: Robert Strausberg (mih.gov

7 Tel: (310) 496-1550

Fmail: Robert_Strausberg (mih.gov

7 Tissue Procurement: DCTD/DFP/Gazdar

CDNA Library Preparation: Life Technologies, Inc.

6 CDNA Library Arrayed by: The T.M. A.G. E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M. A.G. E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
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Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
mail: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases I to 636)

NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)
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                       ttctcctgaaacttcaaggtccctgccagctcctcaagacaatgattttttatctagaaa
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Bonaldo, Ph.D.
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BE551615
BE551615.1 GI:9793227
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/clone="Industrian" / clone="Industrian" / clone="Vector: pT713D-Pac (Pharmacia) with a modified / note=="Vector: pT713D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_CG4 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hypridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clone198 1257096-1258631, 1469064-1470983, and 1475592-1476743); Subtraction by Bento Soares and M. Fatima Bonaldo. "Subtraction by Bento Soares and M. Fatima Bonaldo." CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 455.
Location/Qualifiers Ξ, 1516 1576 1456 1636 1696 1756 1816 acticaaggicccigccagcicctcaagacaaigattittitaictagaaaagcicaagac 1396 tacccggaaatacttgtggtttctagatcaccatctttaaatttacttcaaaataaaagc 1876 atgtaagtgactgtttttcaagaagaaatgtgtttcataaaaggatatttatatctctgt 1936 578 518 458 338 278 218 158 Gaps 98 38 tgttattttatgaagctgcatcactgtcctggaaatcacagttgggatagcaccatttct ggatctcaaaagggctgcattctgtgatcacaagaccactccatgctcttcagcaataata aagcctacaaggacctcaaaagtcagacaattactagacactactgacatccaaggagaa 29.6%; Score 621.8; DB 136; Length 636; 99.5%; Pred. No. 3.2e-126; 1; Indels ? 0; Mismatches /organism="Homo sapiens" /db_xref="taxon:9606"

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1846

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9

AW150819/c DEFINITION

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ORGANISM

ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

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Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. cDNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.lnl.gov/bbrp/image/image.html
Insert Length: 673 Std Error: 0.00
Seq primer: -400P from Gibco.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 592). NCI-CGAP http://www.ncbl.nlm.nih.gov/ncicgap.
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with a modified polylinker; Plasmid DNA from the
normalized library NCI_CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:9606"
/clone="IMAGE:2317103"
/clone_lib="NCI_CGAP_Pr28"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Location/Qualifiers
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/lab_host="DH10B"
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cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-GGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

New-bio.lnl.gov/bbrp/image/image.html

Seq primer: 40UP from Gibco

High quality sequence stop: 402.
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/ Organism="Homo sapiens"

/ Ab_xref="taxon:9606"

/ Clone="ImAGE:2629959"

/ Clone="ImAGE:2629959"

/ Clone="ImAGE:2629959"

/ Lissue_type="well-differentiated endometrial
adenocarcinoma, 7 pooled tumors"

/ lab_host="PHIOB"

/ lab_host="PHIOB"

/ lab_host="Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.75 kb. Life Technologies catalog #:
                                                                                                                                  AW150819 641 bp mRNA EST 03-NOV-1999 xg39f08.x1 NCI_CGAP_Utl Homo sapiens CDNA clone IMAGE:2629959 3' similar to TR:043353 043353 SERINE/THREONINE KINASE RICK.;, mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 641)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Pred. No. 1.7e-123;
9; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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Best Local Similarity 95.9%;
Matches 613; Conservative 9
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/db_xref="taxon:9606"
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Best Local Similarity 98.7%;
Matches 598; Conservative
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this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 985608-986759, 1101192-1101959, and 1217928-1220615). Subtraction by Bento Soares and M. Fatima Bonaldo. " 111 c 128 g 200 t
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100.0%; Pred. No. 1...
0; Mismatches
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AW085560.1 GI:6040712
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                                                                                                               Matches 592;
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Email: Robert_Strausbergenih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
INSERT Length: 885 Std Error: 0.00
Seg primer: -400P from Gibco
High quality sequence stop: 470.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1683
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                                                                                                                                                                                                                                                                                                                                                                                            Score 590.6; DB 110; Length 606;
Pred. No. 2.3e-119;
6; Mismatches 1; Indels 1;
                                                                                                                   /clone="IMAGE:2553606"
/clone_lib="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH108"
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/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Catarrhini, Hominidae, Homo.

1 (bases 1 to 654)

1 (bases 1 to 654)

Nath-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                   BES36247 654 bp mRNA EST 09-AUG-2000 601062632F1 NIH_MGC_10 Homo sapiens CDNA clone IMAGE:3449311 5',
                                                                                                                                          1676 gactatgaacttgttagtaccaagcctacaaggacctcaaaagtcagacaattactagac 1735
                                                                  1736 actactgacatccaaggagaagaatttgccaaagttatagtacaaaaattgaaagataac 1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://lndw12.llnl.gov.co.column: 08
High quality sequence stop: 650.
                                                                                       Length 654;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: ATCC CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: Incyte Genomics, Inc.
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Pred. No. 1.4e-118;
0; Mismatches 11;
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1. .654
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/clone="IMAGE:3449311"
/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE536247.1 GI:9764892
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149 c
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97.6%;
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Matches 638; Conservative
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1 (bases 1 to 647)

Hegde, P., Qi.R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
                                                                                                                                                                                                 AW960501 647 bp mRNA EST 01-JUN-2000 EST372572 MAGE resequences, MAGF Homo sapiens CDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                Assessment of gene expression patterns in a model of colon tumor metactasis using a 19,200 element cDNA microarray inpublished (2000)

Contact: John Quackenbush
The Institute for Genomic Research
772 Medical Center Dr., Rockville, MD 20850, USA
772 Febr: 301 838 3528
Fex: 301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1376 ttatctagaaaagctcaagactgttattttatgaagctgcatcactgtcctggaaatcac 1435
 1924 tttatatctctgttgctttgacttttttttatataaaatccgtgagtattaaagcttwaww 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGTTGGGATAGCACCATTTCTGGATCTCAAAGGGCTGCATTCTGTGATCACAAGACCACT 433
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                   cctggtatagcccagcagtggatccagagcaaaagggaagacattgtgaaccaaatgaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGF"
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128 c 141 g 213 t
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1. .647
                                                                                                                                                                                                                                                       AW960501.1 GI:8150185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: johnq@tigr.org
Plate: 147
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Matches 604; Conservative
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                                                                        1984 raargk 1989
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/organism="Homo sapiens"
/db_xref="taxon:8606"
/db_xref="taxon:8610"
/clone=lib="Nul_CGAP_GB34"
/tissue_type="poorly differentiated adenocarcinoma with signet ring cell features"
/lab_host="DH108"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1: Cloned unidirectionally. Primer: Oligo dT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA160647 645 bp mRNA EST 16-DEC-1996
249011.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone
IMAGE:633044 5', mRNA sequence.
AA160647
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ب
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Pred. No. 7.2e-113;
9; Mismatches 4;
quality sequence stop: 421.
Location/Qualifiers
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97.4%;
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hes 591; Conservative
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Inpublished (1997)
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Tel: (301) 496-1550
Tel: (301) 496-150
Tel: (301) 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI801150 615 bp mRNA EST 14-DEC-1999 to85h04.xl NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2185111 3' similar to TR:043353 043353 SERINE/THREONINE KINASE RICK.; mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 615)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                                                                    aatgattttttatctagaaaagctcaagactgttattttatgaagctgcatcactgtcct
                                   aagaccactccatgctcttcagcaataataaatccactctcaactgcaggaaactcagaa
                                                                                                                                                                                                      AATGATTTTTTATCTAGAAAAGCTCAAGACTGTTATTTTATGAAGCTGCATCACTGTCCT
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AI801150.1 GI:5366622
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AI801150/c
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DEFINITION
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VERSION
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SOURCE
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AUTHORS
TITLE
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1491

1431

2

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/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/lab_host="DHLOB (phage-resistant)"
/lab_host="DHLOB (phage-resistant)"
/lab_host="DHLOB (phage-resistant)"
/cote="Organ: Skin, Vector: pOTBT; Site_1: XhoI; Site_2:
/corsi; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGGG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

(Stratagene) and Superscript II RT (Life Technologies)."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCWB4 row: d column: 04
High quality sequence stop: 636.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF125028 839 bp mRNA EST 24-OCT-2000 601762610F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:4025427 5' BF125028
ccatgaaaatagtggttctcctgaaacttcaaggtccctgccagctcctcaagacaatga 1371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 839)
NIH-MGC http://mgc.nc1.nih.gov/
National Institutes of Health, Mammallan Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AGCAGCGCTGGCGTGGCCATCCGGGGATGGCGCCCTCGTGACTAGTGTTGCGGG 60
                                                                                                                                                                                                                                                                                ttttttatctagaaaagctcaagactgttatttatgaagctgcatcactgtcctggaaa
                                                                                                                                                        1432 tcacagttgggatagcaccatttctggatctcaaaggggctgcattctgtgatcacaagac
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Pred. No. 2.6e-111;
0; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                         1492 cactccatgctcttcagcaataataaatccactctca 1528
                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:4025427"
/clone_lib="NIH_MGC_20"
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94.8%;
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TITLE
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      1312
                                                               361
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Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chissoe, S., Dietrich, N., DuBuque, T., Tevello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags 97044478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; Cloned unidirectionally. Primer: Oligo dT.
Differentiated, post mitotic hWT neurons. Average insert
size: 1.5 kb, Oni. 2AP XR Vector; -5' adaptor sequence: 5'
GANTICGCACGAG 3' -3' adaptor sequence: 5'
GANTICGAG ACTOR ACTO
                                                                                                                              Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
7e1: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -2841 rev2 from Amersham
High quality sequence stop: 373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tgtcaccaatcctttgcagataatgtatagtgtgtcacaaggacatcgacctgttattaa 1011
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                                                                                           Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/db_xref="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:633044"
/clone="IMAGE:633044"
/dev_stage="hNT neurons"
/lab_host="SOLR (kanamycin resistant)"
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Pred. No. 2.4e-112;
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      AA160647.1 GI:1736024
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99.1%;
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                                                                                               ORGANISM
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JOURNAL
MEDLINE
COMMENT
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/clone_limage_num_melanotic melanoma"
/tlssue_type="melanotic melanoma"
/lab_host="bH10B (phege-resistant)"
/note="Organ: skin; Vector: poTB7; site_1: xhoI; site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/RhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
55 a 312 c 294 g 200 t lothers
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0; Mismatches 71; In
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/db_xref="taxon:9606"
/clone="IMAGE:4026156"
                                                                                                                                                                                                                                                                          tch 26.2%;
al Similarity 89.1%;
675; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 1112)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lo Onpublished (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert Strausbergenih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC.Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov

Plate: LLCM856 row: b column: 13

High quality sequence stop: 566.

Location/Qualifiers

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BF125423 GI:10964463
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                                                                                                       accatgaacggggaggccatctgcagcgcctgcccaccattccctaccacaaactcgcc
                                                                                                                       240 GACCIGCGCTACCIGAGCCG-GGCGCCTCTGGCACTGTGTCGTCCG-CCGCCACGCAGAC
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RESULT 13

BF125423

LOCUS

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL COMMENT

AUTHORS REFERENCE

source

FEATURES

240

376 300 436 360 496 420 556 479 919 537 919 594 734, 652 794 710

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399 GAACTTGTTAGTACCAAGCCTACAAGGACCTCAAAAGTCAGACAATTACTAGACACTACT 340
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/clone_lib="BT067"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. conk Library Preparation: M. Bento Soares, Ph.D. conk Library Preparation: M. Bento Soares, Ph.D. DNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NOI-GGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 680 Std Error: 0.00
Seq primer: -40UP from Gibco
Seq primer: -40UP from Gibco
Location/Qualifiers
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                                                                           AI307810 616 bp mRNA EST 08-APR-1999
tb28d07.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2055661 3',
                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 616) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/lab_host="DH10B"
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26.1%; Score 546.8; DB 18
Best Local Similarity 96.4%; Pred. No. 9.4e-110;
Matches 559; Conservative 9; Mismatches 11;
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                                                                                                                                                                                                                                                                                                                                                                                    Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
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/organism="Homo sapiens"
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109 c 11
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Unpublished (1997)
                                                                                                                      mRNA sequence.
AI307810
                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                        human.
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 762)

Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Magai,M.A., and M.A., Bordin,S., Costa,F.F., Nagai,M.A., Costa,C.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deolivelra,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
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/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196, 716 - Ludwig Institute for Cancer Research) profiles
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Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?tl=IL&t2=IL-BT067-023.html
£t3=190199&t4=1)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
1802 atgggtcttcagccttacccggaaatacttgtggtttctagatcaccatctttaaattta 1861
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                                                                       339 GACATCCAAGGAGAAGATTTGCCAAAGTTA-AGTACAAAAATTGAAAGATAACAAACAA
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into the pUC 18 vector. Reverse-transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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ilarity 90.3%; Pred. No. 1.1e-108;
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B1 protein; intracellular mediator; modulator; inflammation; cell death; cell survival pathway; intracellular signalling; AIDS; cancer; human; ss.
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Boldin M, Malinin N,
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This invention describes the isolation of a novel human B1 protein which can interact with, intracellular mediators or modulators of inflammation, cell death and/or cell survival pathways, directly or indirectly. Cells can be modulated or mediated in inflammation, cell death or cell survival pathways or another intracellular signalling activity using B1. Conditions such as AIDS and cancer can be treated using B1. Antibodies, oligonucleotides and ribozymes can also be used to regulate the above cancer treating AIDS, 90pp; English for 3B; Fig 4 pathways Claim

σ :: G; 539 C; 449 BP; 649 A; 452 Sequence 2098

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C77607 to C78448 encode the human cancer associated proteins given in B43398 to B44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antinheumatic; antiarthritic; antinflammatory; antiasthmatic; antiherdic; antibacterial; antiviral; dermatological; antiapterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coaqulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and conditions and diagnosing pathological conditions. Polynucleotides, polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoletic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection,
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                                    diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antiabbetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiliflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss.
acttcaaaataaaagcatgtaagtgactgtttttcaagaagaaatgtgtttcataaaagg 1920
                                                                                                                                                                                       Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cancer associated gene; cancer antigen; detection; cancer;
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modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. C78449 to C78457 and B44240 represent sequences used in the exemplification of the present
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RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-8; NERP-1; diagnosis; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease; ss. 2059 2066 BP. CDNA; 2502 Human RICK coding sequence. (first entry) Z48762 standard; 2072 gaattt 2065 21-MAR-2000 tgaatt 248762; 2007 2067 2060 2000 RESULT Z48762 qq δ . B

Ė Koseki 98US-0069023 (UNMI) UNIV MICHIGAN ž G, Inohara 27-APR-1999; 27-APR-1998; Nunez

Homo sapiens W09955134-A2

04-NOV-1999

WPI; 2000-072163/06. P-PSDB; Y59404.

tions for identifying apoptosis signalling pathway inhibitors for treating diseases $\boldsymbol{\cdot}$ Compositions nseful

Claim 8; Fig 7b; 93pp; English.

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H, Azimzai Y;
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neuronal disorder; ss.
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Au-Young J, Gorgone GA, Yu
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CARD-3; caspase recruitment domain; CARD-4; regulation; detection; caspase activation; detection; screening; therapy; diagnosis; disease; apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex; cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection; hormone-dependent tumour; autolimente disorder; Alzheimer's disease; systemic lupus erythematosis; immune-mediated glomerulonephritis; stroke; Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa;
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This intention describes and CARD-4 polynucleotides and proteins and a partial murine CARD-4L protein and genes. The genes and proteins of partial murine CARD-4L protein and genes. The genes and proteins of caspase activation.

The invention are involved in the requiation of caspase activation.

The caspase recruitment domain (CARD) polynucleotides, polypeptides, homologues and antibodies can be used in screening assays, detection assays, predictive medicine and therapeutic and prophylactic methods of treatment. The methods may be used to diagnose and treat patients which are suffering from a disorder associated with abnormal level or rate of apoptotic cell death, abnormal activity of the TMF receptor complex, abnormal activity of the TMF receptor complex, abnormal activity of a caspase. Diseases that may be treated include cancer (particularly follicular lymphoma, carcinomas associated with mutations at cityity of a caspase. Diseases that may be treated include cancer (particularly follicular lymphoma, carcinomas associated with mutations in p33 and hormone-dependent tumours), autoimmune disorders (e.g. systemic lupus erythematosis, immune-mediated dolomerulonephritis), viral captemic lupus erythematosis, immune-mediated dolomerulonephritis), viral infections, Alzheimer's disease, parkinson's disease, amyotrophic lateral captering and stroke. CARD-3 protein interacts with other cellular proteins, and so can be used for regulation of cellular proliferation and differentiation and captering and stroke. CARD-3 protein interacts with other cellular proteins, and so concompounds which modulate their activity. The CARD-4 qene can express a concompounds which modulate their activity. The CARD-4 qene can express a concompounds which modulate their activity and CARD-4 qene can express a long transcript that encodes CARD-4t, a short transcript that encodes CARD-4t, a short transcript that encodes capted to the capted capted to the capted capted to the capted capted to the capted capted capted capted capted capted capted
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spinal muscular dystrophy; cerebellar degeneration; anaemia; drug; myelodysplastic syndrome; myocardial infarction; cell proliferation; cell differentiation; cell survival; CARD-4L; CARD-4S; CARD-4Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID 228
                                                                                                                  gaacatacctgtaaatcatggtccacaagaggaatcatgtggatcctctcagctccatga
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Sequences F21614 - F22031 represent DNA sequences encoding human proteins B58711 - B59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences F22032 - F22040 and B59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The breast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive, nootropic; antiinflammatory; antiuleer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune hyroiditis, diabetes multiple sclerosis, rheumatoid arthritis and ulcerative colitis; contrological disorders such as myocardial ischaemats, wound healing; contrological
                                                                                                                                                                                                                                                                                                              New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diseases such as cerebral anoxia and epilepsy; and
                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 653; 1299pp; English.
                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
                                                                               08-MAR-2000; 2000WO-US05881
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P-PSDB; B58938.
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WO200055173-A1.
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Sequence 463 BP; 150 A; 92 C; 89 G; 131 T; 1 other;

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DB 21; Length 463;
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Score 454.6; I
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98.7%;
        Best_Local Similarity 98.7
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The invention provides polynucleotides which encode novel protein kinase homologs expressed in various human cells and tissues. The present sequence represents the clone 156108 cDNs fragment derived from a human cDNs library designated THP-1 phorbol LPS. The cDNs encodes a protein kinase which shows homology to the U01064 Dictyostelium Y kinase. Vectors and host cells can be used for recombinant production of the protein kinase homology. The recombinant proteins may be used to raise antibodies for use as anti-kinase therapeutics. Oligonucleotides based on the polynucleotide sequences, i.e. probes and antisense constructs, the petidies and antibodies are claimed to be useful as tools for studying signalling cascades in cells and proteins, and for identifying inhibitors (drugs) to treat diseases and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conditions associated with abnormal kinase expression. Diseases that are claimed to be treatable include human X-linked agammaglobulinaemia, nonspherocytic haemolytic anaemia, artherosclerosis, carcinomas, diabetes, gliomas, restenosis, cholera-based septic shock, etc.
                                                                                                                                                                                                                                                                                                                                   Protein kinase; cell signalling; inflammation; carcinoma; diabetes; human X-linked agammaqibulinaemia; nonspherocytic haemolytic anaemia; artherosclerosis; glioma; restenosis; cholera-based septic shock; U01064 Dictyostelium Y kinase; ss.
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                                                                                                                                                                                                                                                                                                   Clone 156108 cDNA fragment encoding a human protein kinase homolog.
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                                                                  Sequence 210 BP; 74 A; 40 C; 41 G; 55 T; 0 other;
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Pred. No. 1.3e-32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel nucleic acid sequences derived from rat dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocytes stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate anglogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences Zel606-Ze1832 represent CDNA sequences derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      several mouse, rat or human skin cell types. Sequences 261606 261699, 261725-261765, 261802-261811 and 261826 encode proteins with an N-terminal signal sequence, indicating that the proteins are secreted. Sequences 261660-261668, 261766-261780, 261812-261817 and 261827-261829 encode proteins with one or more putative transmembrane domains.
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embryonic skin cell; keratinocyte stem cell; transit amplifying cell; secreted; transmembrane; inflammation; cancer; neurological disease; angiogenesis; tumour vascularisation; growth disorder; developmental disorder; kin wound; hair follicle disorder; anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polynucleotides useful for the treatment of various conditions
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                                                                                                                                                                                                                                                                                                                              dermal papilla; keratinocyte; neonatal foreskin fibroblast;
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98US-0188930.
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09-NOV-1998;
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            Length 1774;
                                                 30;
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                                                   Indels
Score 102.4; DB 21;
Pred. No. 2.7e-11;
                                                 0; Mismatches
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          A.9%;
Similarity 51.8%;
72; Conservative
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                              Best Local Sim
Matches 372;
              Query Match
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                                                                                                                                                                                                                                                                                                                                   The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV) 1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
                                                                                                                                            Kumble KD, . Murison JG;
                                                                                                                                                                                                                                New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 1774;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oligonucleotides for examining expression patterns.
                                                                                                                                            Onrust R, Sleeman M,
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                                                                                                        (GENE-) GENESIS RES & DEV CORP LTD.
                                 15-MAY-2000; 2000WO-NZ00075.
                                                                     99US-0312283
                                                                                                                                          Strachan L,
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                                                                   14-MAY-1999;
23-NOV-2000
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                                              30;
4.9%; Score 102.4; DB 22; Length 151.8%; Pred. No. 2.7e-11;
live 0; Mismatches 316; Indels
                    Best Local Similarity 51.8
Matches 372; Conservative
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The present sequence encodes a murine death associated kinase protein, containing ankyrin repeats, designated DAKAR. The DAKAR polynucleotides can be used to express the polypeptides, and as probes to identify nucleic acids encoding proteins having kinase activity. DAKAR polypeptides and fragmented polypeptides are used for purifying proteins, e.g. to measure protein activity; as quality assurance agents proteins, e.g. to measure protein expired protein protein; as quality of adentify novel molecules involved in signal transduction pathways, and to identify therapeutic compounds which may interfere with apoptosis; as molecular weight and isoelectric focusing markers; as controls for peptide fragmentation; identification of unknown proteins, e.g. up comparison with proteins in databases; and for preparation of antibodies. The antibodies can be used in assays to detect the presence of the protein, and to purify the protein by immunoaffinity chromatography. The antibodies can also be used to block binding of the DAKAR polypeptides to their binding partners. Compounds that inhibit or enhance the kinase activity of DAKAR can be used to treat diseases
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as molecular weight marker and as controls for peptide fragmentation
                                                                                                     947 gaagatgtcaccaatcctttgcagataatgtatagtgtgtcacaaggacatcgacctg 1004
                                                                                                                         Death associated kinase protein containing ankyrin repeats; DAKAR; kinase; quality assurance agent; shelf life; marker; ss.
558 atcgcttacctccctccagagcgaatt---cgtgagaagagccgcttgtttgacaccaaa
                                    cacgatatatatagctatgcagttatcacatgggaagtgttatccagaaaacagcctttt
                                                    DNA encoding a death associated kinase with ankyrin repeats
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98US-0099973.
99US-0119353.
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P-PSDB; Y69163.
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11-SEP-1998;
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                                                                                DB 21; Length 2370;
    production or DAKAR.
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                                      Sequence 2370 BP; 536 A; 660 C; 700 G; 474 T; 0 other;
                                                                              Score 102.4; DB 21;
Pred. No. 2.9e-11;
0; Mismatches 316;
characterized by overproduction or upregulated underproduction or downregulated production of
                                                                             4.9%;
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4.99
Best Local Similarity 51.89
Matches 372; Conservative 287 103 220 527 347 163 407 278 587 à g Qγ Db ò g Ωy g δ qq ŏ a Skin; dermal papilla; keratinocyte; neonatal foreskin fibroblast; embryonic skin cell; keratinocyte stem cell; transit amplifying cell; secreted; transmembrane; inflammation; cancer; neurological disease; anglogenesis; tumour vascularisation; growth disorder; CDNA encoding murine protein kinase/ankyrin homologue, SEQ ID NO:257 (first entry) 27-MAR-2000 261784;

cccagtc---tgcacgtcgacgacagggaacgaatggagctcctggaggaagctaagaag

gggcaggtgtacaaggtgcgccatgtgcactggaagacgtggctcgcgatcaagtgctcg

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Gaps

30;

Length 3516;

Score 102.4; DB 21; Length Pred. No. 3.2e-11; 0; Mismatches 316; Indels

4.98; 51.88;

ctgcccaccattccctaccacaaactcgccgacctgcgctacctgagccgcggggcgctct 346

The invention relates to novel nucleic acid sequences derived from rat dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying calls. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences 261606-261802 represent cDNA sequences derived from several mouse, rat or human skin cell types. Sequences 261606-261649, 261755-261765, 261802-261811 and 261826 encode proteins with an sequence, indicating that the proteins are secreted. Sequences 261650-261668, 261766-261180, 261812-261817 and 261812-261817 encode proteins with one or more putative transmembrane domains. Murison JG; Novel polynucleotides useful for the treatment of various conditions including wounds and cancer -8 follicle disorder; Kumble A, anti-inflammatory; cytostatic; neuroprotective; vulnery; Sequence 3516 BP; 810 A; 886 C; 988 G; 832 T; 0 other; Onrust R, hair 235pp; English. Watson JD, developmental disorder; skin wound; (GENE-) GENESIS RES & DEV CORP 98US-0069726 98US-0188930 99WO-NZ00051 Sleeman M, Claim 1; Page 158-159; WPI; 2000-072177/06 P-PSDB; Y76079 Strachan L, WO9955865-A1 29-APR-1999; 29-APR-1998; 09-NOV-1998; 04-NOV-1999 Mus

oligonucleotides for examining expression patterns.

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The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
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                                                        cagaatatottattggacaatgaatttoatgttaagattgcagattttggtttatcaaag
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                                                                                                                                                 Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV; nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease; ss.
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                            Sequence 3516 BP; 810 A; 886 C; 988 G; 832 T; 0 other;
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                                                                      Score 102.4; DB 22;
Pred. No. 3.2e-11;
0; Mismatches 316;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A single-stranded DNA (or its complementary strand or the corresp. Codouble-stranded DNA) which comprises one of the 7837 "6S" sequences given in T19001-T26837 and which is able to hybridise to part of human genomic DNA, cDNA or mRNA is claimed. The GS (Gene Signature) sequences were obtained from 3'-directed cDNA libraries prepared from various human tissues; synthesis of CDNA was initiated from the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA by using poly(T) as the sole primer since the 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-end of mRNA is repeted courately the relative abundance of is constructed so as to reflect accurately the relative abundance of different mRNAs in the particular tissue from which it was derived. The appearance frequency of a given GS in a cDNA library can be determined (esp. using primers and probes derived from the GS sequences) as a means of diagnosing abnormal cell function or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying gene signatures in 3'-directed human cDNA library for diagnosis of abnormal cell function, by preparing cDNA that reflects relative abundance of corresp. mRNA in specific human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 469; 2245pp; Japanese.
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                                                                                                                                                                                                                    (MATS/) MATSUBARA K.
                                                                                                                                                                                                                                                                                                                                   WPI; 1995-206931/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                                          OKUB/) OKUBO
                                                                                                                                                                                                                                                                                       Matsubara K,
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                                                                                                                                                                      12-NOV-1993;
                             W09514772-A1
                                                                              01-JUN-1995
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The present sequence is that of Genesis clone 971025TRAM004820HT

(Fel) DNA. The translation of the clone (frame 3) is provided in

(TY9154. The polypeptide has kinase activity. The invention

relates to purified murine polypeptides (see Y79152-56) that

have kinase function and isolated nucleic acids encoding them (see

CS 55828-86). The nucleic acids can be used to express the

polypeptides, as probes to identify nucleic acids encoding proteins

having kinase activity, and in assays to identify chromosomes, map

murine genes, and study tumours. Vectors comprising the novel

cn uncleic acids and host cells (bacterial, yeast, plant, insect or

animal) transfected or transduced with the vectors are claimed.

The kinase polypeptides and their fragments are used as mol.wt. and

fragmentation many also have a number of thermanity uses.
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel murine polynucleotides encoding kinase polypeptides, used a probes to identify nucleic acids encoding proteins having kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fragmentation. They also have a number of therapeutic uses, kinases play a central role in cellular signal transduction.
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                                                                                                                                                                                                                                                               Marken JS
                                                                                                                                                                                                                                                               Anderson DM,
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Best Local Similarity 51.9%;
Matches 350; Conservative C
                                                                   98US-0095269
98US-0099973
99WO-US17577
                                                                                                                                                                                       (IMMV ) IMMUNEX CORP.
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P-PSDB; Y79154.
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750 attttggtttatcaaagtggcgcatgatgtccctctcacagtcacgaagtagcaaatctg 809
                                                             cacagaagaagccatttgcagatgaaaagaacatcctacacatcatgatgaaagtggtaa 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New constitutive triple response genes and mutants - isolated from Arabidopsis thaliana, used to produce transgenic plants with improved properties
                                                                                                                   810 caccagaaggaggacaattatttatatgccacctgaaaactatgaacctggacaaaat
                                                                                                                                                          526 gcttgtttgacaccaaacatgatgtatacagcttcgccattgtgatctggggtgtgttta
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118..2583
/*tag= a
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P-PSDB; R80574.
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10-AUG-1992;
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Sequence 3033 BP; 797 A; 605 C; 751 G; 880 T; 0 other;

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                                          0; Mismatches 201;
Score 81.4; DB 16;
Pred. No. 4.1e-07;
3.98;
50.18;
                    Best_Local Similarity 50.1
Matches 202; Conservative
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Description	A82777 Sequence 2	AF027706 Homo sa	AF064824 Homo sa	AF078530 Homo sa	AC004003 Homo sa	AF117829 Homo sa	AR044139 Sequence	AF302127 Mus mus	AJ278016 Homo sapi	I14046 Sequence	I35764 Sequence
ID	A82777	AF027706	AF064824	AF078530	AC004003	AF117829	AR044139	AF302127	HSA278016	114046	I35764
DB	9	88	88	88	82	88		94	92	10	10
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Query Match	9.66	96.2	86.5	77.1	24.6	24.6	10.0	4.9	4.7	3.9	3.9
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AVKHLHIHTPLLDSERKDVLREAEILHKARFSYILPILGICNEPEFLGIVTEYMPNGS
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                                                                                           RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis J. Biol. Chem. 273 (20), 12296-12300 (1998) 981241596 2 (bases 1 to 2501) Inohara, N., Koseki,T., Chen,S., del Peso,L. and Nunez,G. Inohara, N., Koseki,T., Chen,S., del Peso,L. and Nunez,G. Submitted (01-0CT-1997) Dept. Pathlogy, Comprehensive Cancer & Geriatrics Center, 4-131 CCGC 1500 E. Medical Center Dr, Ann Arbor, Parkey Comprehensive Cancer & Geriatrics Center, 4-131 CCGC 1500 E. Medical Center Dr, Ann Arbor, Parkey Comprehensive Center 
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TACCT	caggt CAGGT	gttt GTCTT	ggaat GGAAT	ttaas 	cgcat - - CGCAT	CTTC	gcaga 	tetge 	lll AAAT	ttato TATO	tcaca CACA	agcac AGCAC	ttct	cettg CTTG	ctat	agaggi AGAGG	gtccc 	tatga FATGA
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CTACC	cgccc 11111 cgccc	getge GCTGC	attta ATTTA	tactg TACTG	tgatg TGATG	cctgc	ggaca GGACA	cctct	acctg 	ctatg CTATG	tectt	tttgc 	acaaa ACAAP	gagaa GAGAA	acaga 	catac CATAC	tagte TAGTO	tagaa TAGAA
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ukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
ammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
(bases 1 to 1902)
home,M., Hofmann,K., Burns,K., Martinon,F., Bodmer,J.-L.,
attmann,C. and Tschopp,J.
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| 1125. [1544]
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11545. 1811
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INBLIHRKTEXPDVANPLERRILHETAGVVYIHPMTPPLLHHDLKTQNILLDNEFHV
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TWEVLSRKOPFEDYNPLOIMYSVSGGRPPYINEESLPYDIPHRARMISLIESGWAQN
PDBRRSFLKCLIELEBVLREFEEITFLEAVIOLKKTKLGSVSSAIHLCDKKKMELSLN
IPWHGPODESGSSOLHENGSPETTSRLAPONDFLSRRAADCYFWKLHHOPGNH
SWDSTISGSORAAFCDHKTTPCSSAIINPLZTAGNSFRLOPGIAQQNIGSKREDIVNO
MTBACLNOSIDALLGSPDLINKEDYELVSTREPRISKVRQLLDTTDIQGEEFAKVIVQK
LKDNKQMGLQPYPEILVVSRSPSINLLQNKSM"
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McCarthy,J.V., Ni,J. and Dixit,V.M.
RIP2 is a novel NF-kapaB-activating and cell death-inducing kinase J. Biol. Chem. 273 (27), 16968-16975 (1998)
                                                                                                                                                                                                                                                                                                                                           AF078530 1623 bp mRNA PRI 28-JUL-1998 Homo sapiens receptor interacting protein 2 (RIP2) mRNA, complete
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1623)
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/db_xref="taxon:9606"
1 .1623
/gene="RIP2"
/function="activtes NF-kappaB"
/function="induces cell death"
/note="RIP2"
/choclion="induces cell death"
/choclion="induces cell death"
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Pred. No. 1.8e-277;
0; Mismatches 4;
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Submitted (115-JUL-1998) Molecular On Way, South San Francisco, CA 94080, Location/Qualifiers
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                                            tattttatgaagctgcatcactgtcctggaaatcacagttgggatagcaccatttctgga 1459
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 116650)
Ozersky,P., Holmes,A. and Broy,M.
The sequence of Homo sapiens BAC clone CTA-437L15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Genetics,
Park Avenue, St. Louis,
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Park Avenue, St. Louis,
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Homo sapiens BAC clone CTA-437LL5
AC004003
AC004003.1 GI:2772557
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University, 4444 Forest
4 (bases 1 to 116650)
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Submitted (15-JAN-1998)
University, 4444 Forest
3 (bases 1 to 116650)
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Waterston, R.
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/rpt_f.amlly="Alu"
7110. 8040
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/gene="WUGSC:H_RG437L15.1"
/gene="WUGSC:H_RG437L15.1"
10in/7872. 8044,12642. 12795,15154. 15309,19584. 19741,
21552. 21601,22478. 22639,29890. 29975,33855. 33944,
36395. 36488,39123. 39284,39881. 40218)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE INFORMATION:
Clone CTA-437L15 is from a release of the human BAC library
CITB-HS-A. The library contains cloned DNA from human sperm.
Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J.
Kim et al., Genomics 34:213-8 (1996). The clone is available from
VECTOR: pBeloBAC11
                                                                                                                                                     the entire insert of this
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                                                                                                                                                                     clone sections once, or longer because we only sequence overlapping between neighboring data submissions.
                                                                                                                                                                                                                                                                              This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is CTA-237G1. The actual start of
this clone is at base position 1 of CTA-437L15; actual end is at
116650 of CTA-437L15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This chromosome 8 clone was provided by Dr. Patrick Concannon (patcon@vmmc.org) at the Virginia Mason Research Institute.
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Location/Qualifiers
1. .116650
/organiam="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="8"
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
                                                                                                                                                        NOTICE: This sequence may not represent
                                                                          Center project name: H_RG437L15
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6133. .6433
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/clone_lib="CITB-HS-A"
150. .530
/rpt_family="L1"
498. .649
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3845. .4563
/rpt_family="L1"
5641. .6075
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/rpt_family="MaLR"
3188. .3340
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/rpt_family="L1"
3605. 3775
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/rpt_family="L1"
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Homo sapiens 8q21.3: RICK gene, complete sequence.
AF117829
AF117829.1 GI:4151947
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Pred. No. 3.7e-82;
9; Mismatches 3; I
/rpt_family="MER2_type"
35994, .36286
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/rpt_family="Alu"
44088. .44386
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37488. 3727.
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41954. .4200.
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8297. .38599
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37862. .38161
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42596. .42777
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Matches 513; Conservative
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81466. .31688
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29435. .29752
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1433. .11538
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ORGANISM Homo sapiens ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 320250) AUTHORS Platzer, M. and Varron, R. TITLE Direct Submission JOURNAL Submitted (30-DEC-1998) Genome Analysis, Institute of Molecular Blotechnology, Beutenbergstrasse 11, Jena 07745, Germany COMMENT This sequence is part of a larger genomic contig. The start of this	sequence is directed towards the centromere. The end of this sequence (32001. 320250) overlaps with the start of the neighbouring Acc_number AF049895 (1250). FEATURES 1320250 Occation/Qualifiers 1320250 Accapanism="Homo sapiens" /cho_xref="taxon:9606"	/map="8q21.3" source 1.37184 /organism="Homo sapiens" /db_xref="taxon:9606" /db_xref="taxon:9606" /clone="p64M4" repeat_region complement(572704) /rpt_family="MIR"	repeat_region (rpt_family="MIR" repeat_region (7pt_family="MIR" repeat_region 25382864 repeat_region 25382861 repeat_region complement(26952845) repeat_region 29133485 repeat_region 29133485 repeat_region 29133485	repeat_region //rpt_family="MLTIA1" / rpt_family="L2" / rpt_family="L2" repeat_region //rpt_family="MLTIA1" repeat_region //rpt_family="MLTIA1" repeat_region //rpt_family="(rAR)n" / rpt_family="(rAR)n" / rpt_family="(rAR)n" / rpt_family="(rARG)n" / rpt_family="MER53" repeat_region //rpt_family="MER53" repeat_region //rpt_family="MRTA" repeat_region //rpt_family="MLR" repeat_region //rpt_family="MLR" repeat_region //rpt_family="MLR" repeat_region //rpt_family="MLR" / rpt_family="MLR" / rpt_family="MLR"

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Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3559) Chen, L., Haider, K., Cariappa, A., Rowitch, D. and Pillai, S.
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Mus musculus PKC-regulated kinase PKK mKNA, complete cds.
AF302127
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Au-Young, J., Bandman, O., Hawkins, P.R.
Human kinase homologs
Patent: US 5817479-A 31 06-OCT-1998;
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rpt_family="THE1C-internal"
 /rpt_ram...
44392. .45158
/rpt_family="LlMA4A"
.complement(45759. .46216)
family="LlPA7"
                                                                                                                                            complement (49170. .49277)
/rpt_family="MIR"
complement (49409. .50232)
/rpt_family="LiPA2"
50233. .50476
                                                                                                                                                                                                                                                                                                    v-"THE1C"
                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="L2"
complement(55316. .55371)
/rpt_family="L2"
i5545. .55878
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62004. .62295
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complement(50588, .50644)
/rpt_family="MiR"
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/rpt_family="THE1C"
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                                                                                /rpt_family="L1MA4A"
47693. .47955
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18227. .48421
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62833. .145579
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rpt_family="MLT1A2"
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62427. .67614
/rpt_family="AluJo"
44392. .45758
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/rpt_family="LlME"
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7436, .57481
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/rpt_family="L2"
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DFGLAKCNGMSHSQDLSMDGLFGTIAYLPPERIREKSRLFDTKHDVYSFAIVIWGVLT
QKRPPADEKNILHIMMKVVKGHRPELPPICRRRPRACASLIGLMQRCWHADPQVRPTF
QETISFETBLCEKPDEEVKDLAHEPGEKSSLESKERARRESSRLKRASAPPFDNDCSL
SELLSQLDSGTSQTLEGPEELSRSSECKLFSSSGGRLSGVSSVDSAFSSRGLSLS
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GQEECVKWLLLNNANPNLTNRKGSTPLHMAVERKGRGIVELLLARKTSVNAKDEDQWT
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LOGKDAWLEHTAANGGHLEPTVKLLAKQPGVSVNAQTLDGRTPLHLAAQRGHYRVARI
LIDLCSDVINICSLQAQTPLHVAAETGHRSTARLLLHRGAGKEALTSEGYTALHLAAQN
GHLATVKLLIEEKADVARGPLNOTALHLAAARGHSEVVEELVSADLIDLSDEGGLSA
LHLAAQGRHSQTVETLLKHGAHINLQSLKFQGGQSSAATLLRRSKT"
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KTWLAIKCSPSLHVDDRERMELLEEAKKMEMAKFRYILPVYRICQEPVGLVMEYMETG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLEKLLASEPLPWDLRFRIVHETAVGMNFLHCMSPPLLHLDLKPANILLDAHYHVKIS
  PKK, a novel ankyrin repeat-containing protein kinase regulated by
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                                                              Chases 1 to 3559)
Chen.L., Haider.K., Cariappa, A. and Pillai, S.
Chen.L., Haider.K., Cariappa, A. and Pillai, S.
Direct Submission
Submitted (01-2EP-2000) Cancer Center, Massachusetts General Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                        /product="PKC-regulated kinase PKK"
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/db_xref="G1:11120431"

    3559
    /organism="Mus musculus"
/strain="BALB/c"

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                         protein kinase C-beta
Unpublished
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Similarity 51.8%;
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EECAKWILLINNANPNISNRRGSTPLHMAVERRVRĞVVELLLARK I SVNAKDEDQWTAL
HFAAQNGDESSTRLLEKNASVNEVDFEGRTPWHYACQHGGRIYRTLILRRGYDVSLQ
RENAWLPLHYAAWGGHLPIYKLLAKQPGVSVNAQTLOGRTPLHLAAQRGHYRVARILI
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LATVKLLVEEKADVLARGPLNQTALHILAAAHGHSEVVEELVSADVIDLFDEQGLSALH
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SLEKLLASEPLPWDLRFRIIHETAVGMNFLHCMAPPLLHLDLKPANILLDAHYHVKIS
DFGLAKCNGLSHSHDLSMDGLFGTIAYLPPERIREKSRLFDTKHDVYSFAIVIMGVLT
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OGTIFSTEDBLCERPDDEVKFAHDLVKSPPERPSSEVVPARKRRASAFFDNNYSLSE
CLISOLDSGVSQAVGEBELSRSSSERIPSSGSGKRLSGVSSVDSAFSSRGSISLSF
REPSTSDLGTTDVQKKKLVDAIVSGDTSKLMKILQPQDVDLALDSGASLLHLAVEAGQ
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 3879)
Babr.C.; Rohwer, A.; Stempka, L.; Rincke, G.; Marks, F.; and
Gschwendt, M.

DIK, a Novel Protein Kinase That Interacts with Protein Kinase
J. Biol. Chem. 275 (46); 36350-36357 (2000)
                                                                                                                                                                 cacgatatatatatctatgcagttatcacatgggaagtgttatccagaaaacagcctttt 946
602 ATCGCTTACCTCCTCCAGAGCGAATT -- - CGTGAGAGGAGCCGCTTGTTTGACACCAAA 658
                                                                                                                                                                                                            659 CATGATGTATACAGCTTCGCCATTGTGATCTGGGGTGTGCTTACACAGAAGAAGCCATTT 718
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                                                                     attatttatatgccacctgaaaactatgaacctggacaaaaatcaagggccagtatcaag
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3838. .3843
/gene="dik"
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Homo sapiens mRNA for protein kinase (dik gene).
AJ278016
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/db_xref="taxon:9606"
/clone_lib="HaCaT"
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Ecker,J.R. and Kieber,J.J.
Constitutive triple response gene and Patent: US 544166-A 1 22-AUG-1995;
Location/Qualifiers
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Sequence 1 from patent US 5-
114046
114046.1 GI:996469
 4.78;
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            Best_Local Similarity 51.4
Matches 369; Conservative
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(Constitutititation of the patent: US 5602322-A 1 11-FEB-1997;

Location/Qualifiers

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Pred. No. 7.6e-05;
0; Mismatches 201;
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 DB 10;
 Score 81.4; DB 10 Pred. No. 7.6e-05,
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Best Local Similarity 50.1%;
Matches 202; Conservative
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Similarity 50.1%;
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NGCNTGRAKAERGGFDMPSGGGGGDHRLNNOPNRYGNNAT ASSLGLORGSSGSFGE
SSLSGDY WHPILSAAANE IESVGFPODGFRLGFGGGGGDLRIOMADSAGGSSGKFG
SSLSGDY SAMPTLESSAAANE IESVGFPODDGFRLGFGGGGGDLRIOMADSAGGSSGKR
MAQOTEESVOLOLALARLSSEATCANDPNR-LDPVPDESALRYSPSSAETVSHFRWYN
GCLSYTOKVPDGFYMMGLDPY IWTLCI DLHESGRIF PS IESLAAVDSGYDSSLENI IV
DRRSDPAFKELHNRVHDISCSCITTKEVVDQLAKLICNRMGGPVIMGEDELVPMWKC
INGLAEFRYVVPTGSLSVGLCRHRALLFKVLADIIDLFCRIAKGCKYCNRDDAASCL
VRFGLDREYLVDLVGKPGHLWEPDSLLNGPSSISISSPLRFPRRFYVPERLLAK
QYFSDSQSLINLYPDPASDDMGFSFFFHRQYDDGFRDALARGGGSLPPSANMPPDNM
MRASNOJEBAPMARP ISQPYDNRARREJCLGGDDMIIPWCDLNIKEKIGAGSFGTVH
RAEWHGSDVAVKILMEQDFHAERNNEFLREVAIMKRLRPPNIVLFMGAVTOPPNLSIV
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicoryledons; core eudicots; Rosidae; eurosids II; leassicales; Brassicaceae; Arabidopsis.
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ATIMDLLRPLIKSAVPPPNRSDL"
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                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana negative regulator of the ethylene response pathway (CTR1) mRNA, complete cds.
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                                                                                                                                                                  660 acctgcacaatatgactcctcctttacttcatcatgacttgaagactcagaatatcttat 719
540 ttactgaatacatgccaaatggatcattaaatgaactcctacataggaaaactgaatatc 599
                                                                                                             600 ctgatgttgcttggccattgagatttcgcatcctgcatgaaattgcccttggtgtaaatt
                                       1988 TGACAGAATATTTGTCAAGAGGTAGTTTATACAGACTTTTGCATAAAAGTGGAGCAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3702"
/de_zstage="dark grown seedling (3 days old)"
/tissue_type="hypocotyl and cotyledon"
118. .2583
                                                                                                                                                                                                                                                                                 2168 TIGACAAAAATATACAGTCAAGGTTTGTGATTTTGGTCTCTC 2210
                                                                                                                                                                                                                                                   /organism="Arabidopsis thaliana"
/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="protein kinase"
/protein_id="AAA32779.1"
/db_xref="GI:166680"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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/gene="CTR1"
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                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
MEDLINE
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KEYWORDS
SOURCE
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Score 81.4; DB 13; Length 3033; Pred. No. 7.6e-05;

3.9%; 50.1%;

Best Local Similarity

Query Match

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Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
1; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 2767)
Kannan,P. and Giovannoni,J.J.
Ethylene-inducible tomato CTRI-like protein kinase
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AF110519 2767 bp mRNA PLN 28-JAN-1999
Lycopersicon esculentum ethylene-inducible CTR1-like protein kinase
mRNA, complete cds.
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protein_id="AAD10057.1"
/db_xref="G1:4193950"
/translation="MSGRRSSYTLLNQIPNDNFFQPPAPKFSAGAGVLPYGESSSAEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRGKVFDLDLMDQRMMQSHNRVGSFRVPGSIGSQKQSTEGSFRGSSLSGENYVGTSFG
HKNECGSSYARNWAQQTEESYQLQLALAIRLSEATCADSPRFLDPYTDVLASRDSD
STABAVTMSHRLMINGCMSYFDKVPDGFYMIYGMDPYWALCSVVQESGRIPSIESLK
AVDPSKAAPSVEVILIYURCNDLSLKELQNRIHSISPSCITTKEAVDQLAKLVCDHMGGA
APAGEEELVSMSKGCSNDLKDRFGTIVLPIGSLSVGLCRHRALLFRVLADIIDLPCRI
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Submitted (02-DEC-1998) Horticultural Sciences, Texas A&M
University, Mail Stop 2133, College Station, TX 77843-2133, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                            1928 GCCACCCTAACATTGTTCTCTTCATGGGTGCGGTCACTCAACCTCCAAATTTGTCAATAG 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1808 CTGTCCACCGTGCTGAGTGGCATGGCTCGGATGTTGCTGTGAAAATTCTCATGGAGCAAG 1867
                                                                                                                                                                                             1868 ACTICCATGCTGAGCGTGTTAATGAGTTCTTAAGAGGGTTGCGATAATGAAACGCCTTC 1927
                                                                                                                                                                                                                                                                                                                                                                                             599
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360 ccgcccgccacgcagactggcgcgtccaggtggccgtgaagcacctgcacatccacactc 419
                                                                                                                               420 cgctgctcgacagtgaaagaaaggatgttttaagagaagctgaaattttacacaaagcta
                                                                                                                                                                                                                                                              gatttagttacatttttccaattttgggaatttgcaatgagcctgaatttttgggaatag
                                                                                                                                                                                                                                                                                                                                                                                          540 ttactgaatacatgccaaatggatcattaaatgaactcctacataggaaaactgaatatc
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1988 TGACAGAATATTTGTCAAGAGGTAGTTTATACAGACTTTTGCATAAAAGTGGAGCAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         600 ctgatgttgcttggccattgagatttcgcatcctgcatgaaattgcccttggtgtaaatt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2168 TTGACAAAAATATACAGTCAAGGTTTGTGATTTTGGTCTC 2210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tggacaatgaatttcatgttaagattgcagattttggtttatc 762
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/organism="Lycopersicon e:
/organism="Achopersicon e:
/oultivar="Alisa Craig"
/db.xref="taxon:4081"
/chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 2767)
Kannan, P. and Giovannoni, J.J.
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/db_xref="taxon:4081"
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Bugnollophyta; eddlcotyledons; core eddlcots; Asteridae; euasterids
1; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 2829)
Zegzouti, H., Jones, B., Frasse, P., Marty, C., Maitre, B., Latch, A., Pech, J.C. and Bouzayen, M.
Ethylene_regulated gene expression in tomato fruit:
characterization of novel ethylene-responsive and ripening-related genes isolated by differential display
Plant J. 18 (6), 589-600 (1999)
                                                        VVSÄ I PSEELDLDVEEFNI PWNDLVLMEK I GAGSFGTŸHRGDWHGSDVAVK I LMBQDF
HAERLKEFLREVA I MKRLRHPNI VLFWGAV I QPPNLS I VTEYLSRGSLY RLLHKPGAK
KVLDERRPLCLAY DVANGMNY LHKRNPPI VHRDLK SPNLLVDKKYTVK I CDFGLSRFK
                    RYRQVEPTTDFRAAADGDAGQSDRSCIDRNNVVSSSSNRDEISQLPPPLINAWKKGRD
KESQLSKMYNPRSMLNPVNMDEDQVLVKHVPPFREDAQSPWTRPDTVNDTRFLAGGGH
                                                                                                                ANTFLSSKTAAGTPEWMAPEVIRDEPSNEKSDVYSFGVILWELATLQQPWNKLNPPQV
IAAVGFNRKKLDIPSVLNPRVAIIIEACWANEPWKRPSFSTIMDMLRPHLKSPLPPPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF096250 2829 bp mRNA PLN 02-AUG-1999
Lycopersicon esculentum ethylene-responsive protein kinase TCTR1 (ERS0) mRNA, complete cds.
AF0965250 GI:5669641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (02-0CT-1998) Lab 'ETHYLENE', ENSAT-INRA, Avenue de
1'Agrobiopole BP 107, Auzeville Tolosan, Castanet Tolosan cedex
31326, France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1780 AAGGAATTTTTGAGGGAGGTTGCAATTATGAAGCGGTTGCGACATCCAAATATTTGTACTT 1839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cctitacttcatcatgacttgaagactcagaatatcttattggacaatgaatttcatgtt 739
                                                                                                                                                                                                                                                                                                                              440 aaggatgitttaagagaagcigaaattitacacaaagciagattiagtiacattiticca 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          620 agatttcgcatcctgcatgaaattgcccttggtgtaaattacctgcacaatatgactcct
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0
                                                                                                                                                                                                                                                  Length 2767;
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                                                                                                                                                                                                                                                Score 78.2; DB 12;
Pred. No. 0.00028;
0; Mismatches 153;
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2080 AAGATCTGTGATTTTGGTCTTTC 2102
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52.6%;
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                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                          Matches 170;
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.2829
 /organism="Lycopersicon esculentum"
 /cultivar="Evita"

source

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/product="ethylene-responsive protein kinase TCTR1"
/product="ethylene-responsive protein kinase TCTR1"
/do_xref="G1:5666406.1"
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STASAVTMSHRUMINGCMSYFDKVPDGFYWIYGMDPYWALCSVVQESGRIPSIESLR
APPSFARDSYEVILIDRCNDLSLKELDNRIHSISSSCITTRARDVQLARKVCVDHMGGA
APAGEBELVSMSKGCSNDLKDRFGTTYLPIGSLSVGLCRHRALLFKVLADIIDLFCRI
AKGCKYCNSSDASSCLVKFEHDREYLVDLIGKPGVLSEPDSLLNGPSSISIPSPIRF
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SSNRDEISQLPLPPLNAWKKGRDKESQLSKMYNPRSMLNPVNMDEDQVLVKHVPPFRE
DAGSPYTRPDTVNDTRFLAGGGHVVSA.TPSEELDLDVEEFR TPWNDLILMEK.GAGSF
GTVHRGDMHGSDVAVKILMEQDFHAERLKEFLREVAIMKRLRHPNIVLFMGAVIQPPN
LSIVTEYLSRGSLY.TRLHKPGAREVLDERRRCKMAYDVANGMNYLHRRNPIVHRDLK
SPNLLVDKKYTVKICDFGLSRFKANTFLSSKTAAGTPEWMAPEVIRDEPSNEKSDVYS
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                                                                                                                                                                                                                                                                                                              /note="serine/threonine kinase; similar to Arabidopsis thaliana negative regulator of the ethylene response pathway encoded by GenBank Accession Number L08789"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1835 AAGGAATTTTTGAGGGAGGTTGCAATTATGAAGCGGTTGCGACATCCAAATATTGTACTT 1894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   500 attitigggaattigcaatgagcctgaattitigggaatagttactgaatacatgccaaat 559
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Pred. No. 0.00028;
0; Mismatches 153;
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2543. .2829
/tissue_type="green fruit"
/dev_stage="late immature"
/note="ethylene-treated"
                                                                                                                                                       'note="ethylene-inducible"
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/gene="ER50"
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                                                                                                                                /gene="ER50"
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Matches 170; Conservative
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AF110518
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67...z.556
/note="protein kinase homolog; ethylene and fruit ripening
inducible CTR1-like protein kinase; TCTR1"
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AKGCKYCNSSDASSCLVRFEHDREYLVDLIGKPGVLSEPDSLVNGPFSISIPSPLRFP
RYRQVEPTIDFRSLAKQYFLDSQSLNILFDDSSSAGAAADGDAGQSBREGCIDRNNVVSS
SSNBEISQPPPLNAKKGRDKESQLSKWYNPRSMLNPVNMDEDQVLVKHVPPFRE
DAQSPWTRPDTVNPTRALAGGGHYVSA IPSEELDLDVEEFNIFWNDLVLMEK GGAGSF
GTVHRGDWHGSDVAVKILMEQDFHAERLKEFLREVAIMKRLRHPNIVLFMGAVIQPPN
                                                                                                                             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids 1; Solanales; Solanaceae; Solanum; Lycopersicon.

I (bases 1 to 2813)

Kannan, P. and Glovannoni, J.J.

Ethylene-inducible tomato CTR1-like protein kinase
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SPULLYDKKYTVKICDFGLSRFKANTFLSSKTAAGTPEWMAPEVIRDEPSNEKSDVYS
FGVILWELATLQOPWNKLNPPQVIAAGFNRKKLDIPSVLNPRVAIIIEACWANEPWK
RPSFSTIMDMLRPHALDQOPWNGCHTDWQLLS"
567 c 672 g 852 t
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HKNEGCGSSVARNWAQQTEESYQLQLALAIRLSSEATCADSPNFLDPYTDVLASRDSD
STASAVTMSHRLWINGCMSYFDKVPDGFYWIYGMDPYVWALCSVVQESGRIPSIESLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVDPSKAPSVEVILIVRCNDLSLKELQNRIHSISPSCITTKEAVDQLAKLVCDHMGGA
                                                                                                                                                                                                                                                                                                                                                                                      Submitted (02-DEC-1998) Horticultural Sciences, Texas A&M University, Mail Stop 2133, College Station, TX 77843-2133, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2089 CCCATTGTGCACCGAGATTTAAAATCTCCCAAAGTAGACAAAAAATATACAGTG 2148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="ethylene-inducible CTR1-like protein kinase"
/protein_id="AAD10056.1"
/db_xref="GI:4193948"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1909 TTTATGGGTGCTGTCATTCAGCCACCAAATTTGTCCATAGTCACGGAATATTTATCGAGA 1968
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/organism="Lycopersicon esculentum"
/cultivar="Ailsa Craig"
/db_xref="taxon:4081"
/chromosome="2"
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illarity 52.6%; Pred. No. 0.00028;
Conservative 0; Mismatches 153;
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                                                                                                                                                                                                                                                                                                              2 (bases 1 to 2836)
Kannan, P. and Giovannoni, J.J.
Direct Submission
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                                                                                                             Lycopersicon esculentum
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AF110518.1 GI:4193947
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Best Local Similarity
Matches 170; Conserv
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Search completed: Jure 13, 2001, 17:39:55 Job time: 9374 sec

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1 MNGEAICSALPTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSER 60
                                                                                                                                                                             Sequence 2, A Sequence 10, Sequence 37,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Bertin, John
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: GENES ENCODING CASPASE RECRUITMENT
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
NUMBER OF SEQUENCES: 4
CORRESPENDENCE ADDRESS:
ADDRESSE: Fish & Richardson P.C.
STREET: 25 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.6%; Score 2817; DB 3;
99.6%; Pred. No. 1.5e-260;
live 0; Mismatches 2;
                                                                                                                                                                                             DCT-USS5-05088-10
US-08-701-191A-37
US-09-035-706-6
US-08-955-841-6
US-08-571-758-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: Diskette
COMPUTER: Mindows 95
SOFTWARE: FastESO for Windows Version 2.0b
CURRENT APPLICATION DATA:
FILING DATE: US/09/019,942
FILING DATE: 06-FEB-1998
                                                                                   US-08-473-553A-5
US-08-587-889-2
US-08-980-060-5
US-09-307-185-5
PCT-US96-09193-2
                                                                                                                                                                                                                                                                                                                              US-08-909-983-11
US-08-587-680A-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09019942 Patent No. 6033855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
ATTORNEY/AGENT INFORMATION:
MANE: Meiklejohn, Ph.D., An.
REGISTRATION NUMBER: 35,283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 540 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches 538; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 06-FEB-:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: DC.
STATE: MA
COUNTRY: USA
COUNTRY: USA
TO: 02110-2804
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TOPOLOGY:
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Sequence 185, App
Sequence 15, Appl
Sequence 9, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 2, Appli
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762.306 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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Maximum Match 100%
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33.6%; Pred. No. 2.4e-46;
.lve 64; Mismatches 154; Indels 116; Gaps
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                        KDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPL
                                                                                       SVSQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEI
                                                                                                                                                                                          241 SVSQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEI
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MNGEAICSALPTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSER
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APPLICANT: Steamen, Lorna
APPLICANT: Steamen, Matthew
APPLICANT: Steamen, Matthew
APPLICANT: Oncust, Rene
APPLICANT: Oncust, Rene
APPLICANT: ONCUST, Rene
TITLE OF INVENTION: Compositions Isolated From Ski
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ. ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 334, Application US/09188930A Patent No. 6150502 GENERAL INFORMATION:
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Best Local Similarity
Matches 169; Conserv
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LENGTH: 787
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ORGANISM:
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                                                                                                                                                                       SWDSTIS--GSQRAAF------CDHKTTPCSSAIINPLSTAGNSERLQPGIAQQW 439
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                                                                        QGHRPVINEESLPYDIPHR---ARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEI 300
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                                                G--GTIIYMPPENYEPGOKSRA-SIKHDIYSYAVITWEVLSRKOPFEDVTNPLQIMYSVS
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; Pred. No. 8.9e-43;
64; Mismatches 159; Indels 118;
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APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Lorna
APPLICANT: Stream, Matthew
APPLICANT: Ornust, Rene
APPLICANT: Ornust, Rene
TITLE OF INVENTION: and Methods For Their Use
TITLE OF INVENTION: and Methods For Their Use
FILE REPERENCE: 11000.1011c1
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEO ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 185
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Best Local Similarity 32.5%;
Matches 164; Conservative 64
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1larity 25.7%; Pred. No. 9.1e-29;
Conservative 84; Mismatches 183;
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APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REPERENCE: PHM. 70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6096539
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ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 132; Conserv
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US-09-329-418-9
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                                   300 ITFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPE 359
                                                                       ---SETEDLCEKPDEEVK---DLAHEPGEKSSLESKSEARPESSR 321
                                                                                                                                                                                                              379 VSSVDSAFSSRGSLSLSFEREASTGDLGPTDIQKKKLVDAII-----SGDTSRL----M 428
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                                                                                                                                           322 LKRASAPPFDNDCSLSELLSQLDSGIFPRLLKGPEELSRSSSEC---KLPSSSSGKRLSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02110-2804

COMPUTER REAGABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
239 VKGHRP----ELPPICRPRPRACASLIGLMQRCWHADPQVRP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street, Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         00383/026001
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Leder, Philip
APPLICANT: Seed, Brian
APPLICANT: Stanger, Ben Z.
APPLICANT: Lee, Tae-Ho
APPLICANT: Kim, Emily
TITLE OF INVENTION: CELL DEATH PROTEIN
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/444,005
                                                                                                                                                                                                                                                  438 QWIQSKREDIVNQMTEACLNQSLDA 462
                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/08444005 Patent No. 5674734 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Clark Paul T.
REGISTRATION NUMBER: 00.164
REFERENCE/DOCKET NUMBER: 0038
TELECOMMUNICATION INFORMATION:
TELEPPHONE: 617/542-5070
TELEPAX: 617/542-8906
                                                                                                                                                                                                                                                                          ::|:|::|::|429 KILQPQDVDLVLDSSASLLHLAVEA
                                                                                                                                                                              391 NHSWDSTIS--GSQRAAF-----
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INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 656 amino acids
                                                                                                         360 TSRSLPAPQDNDF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; MOLECULE TYPE: protein US-08-444-005-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
                                                                       281 IT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
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COUNTRY:
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193 248 248 249 VINE--ESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEP-VLRTFEEITFLEA 305 301 306 VIQLKK-----TKLQSVSSAIHLC------DKKKMELSLNIPVNHGPQEESCGSSQ 350 351 LHENSGSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHK 410 71 HKARFSYIFPILGICNEPEF----LGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRIL 125 126 HEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAP 185 244 245 GHRPVINEESLPY---DIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEE-- 299 65 ASLDNEFVLRLEGVIEKVNWDQDPKPALVTKFWENGSLSGLLQSQCPRP---WPLLCRLL 121 Gaps PTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDVLREAEIL 70 180 -GGTLGYLAPELF-VNVNRKASTASDVYSFGILMWAVLAGRE-VELPTEPSLVYEAVCNR 80 GIIIEEGNYSLVMEYMEKGNLMHVL--KTQI-DVPLSLKGRIIVEAIEGMCYLHD--KGV 194 PPE----NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRP 302 VASLKKEYPDOSPVLQRMFSLQHDCVPLPPSRSNSEQPGSLHSSQGLQMGPVEESWFSS-EGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSV-SQ LHHDLKTQNILLDNEFHVKIADFGLSKWRMMS-LSQSRSSKSAP-----EGGTIIYM

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FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
                                                                                                                                                                                      ; OTHER INFORMATION: Delta Death Domain US-09-329-418-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  300 ITFLEAVIQLKKTKLQSVSSA 320
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                                                                                                                                                                                                                                                                                                            Matches 103; Conservative
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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US-09-329-418-5
                                                                                                                    LENGTH: 420
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                                                                                                                                                                              FEATURE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 ASLDNEFVLRLEGVIEKVNWDQDPKPALVTKFWENGSLSGLLQSQCPRP---WPLLCRLL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 GHRPVINEESLPY---DIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEIT 301
                        -----LCDKKKMELSL 333
                                                              354
                                                                                                                                        EEPPSSVPKKCPSLTKRSRAQEEQVPQAWTAGTSSDSMAQPPQTPETSTFRNQMPSPTST 414
                                                                                                                                                                              -----FMKLHHCPGNHSWDSTISGSQRAAFC 407
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                                                    NAAVSTVKDFLSQLRSSNRRFSIPESGQGGTEMDGFRRTIENQHSRNDVMVSEWLNKLNL
                                                                                                                                                                                                                  GTPSPGPRGNQGAERQGMNASCRTPEPNPVTGRPLVNIYNCSGVQVGDNNYLTMQ-
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                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09329418
Patent No. 6096539
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
ITTLE OF INVENTION:
FILE REFERENCE: PHM.70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13.7%; Score 388; DB 3; I
llarity 32.0%; Pred. No. 1.1e-28;
Conservative 62; Mismatches 125;
                          -- TKLQSVSSAIH-
                                                                                                                                                                                                                                                          408 DHKTTPCSSAIINPLSTAGNSERLQ--PGIAQQ 438
                                                                                                                                                                                                                                                                                470 --QTTALPTAGLAP---SGKGRGLQHPPPVGSQ 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-329-418-8; Sequence 8, Application US/09329418; Patent No. 6096539
                                                                                                                                                                                362 -RSLPAPQDNDFLSRKAQDCY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 FLEAVIQLKKTKLQSVSSA 320
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Best Local Similarity
Matches 102; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
LENGTH: 518
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US-09-329-418-3
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336 NRQNRPSLAE--LPQAGPETPGLEGLKELMQLCWSSEPKDRPSFQECLPKTDEVFOMVE- 292
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                                                                                                                                                                                                                                                     ASLDNEFVLRLEGVIEKVGGSSQDPK-PALVTKFMENGSLSGLLQSQCPRP---WPLLCR 120
                                                                                                                                                                                                                                                                                                                    ILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQGHRPVINEESLPY---DIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEE 299
                                                                                                                                                                                                                71 HKARFSYIFPILGI-----CNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFR 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14 PLVSIEELENQELVGKGGFGTVFRAQHRKWGYDVAVRIVN-----SKAISREVKAM 64
                                                                                                      11 PTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDVLREAEIL 70
                                                                                                                                      184 APEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 420;
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Patent No. 6096539
GENERAL INFORMATION:
APPLICANT: ZENECA LIMITEd
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 13.6%; Score 385; DB 3; 1
Best Local Similarity 31.7%; Pred. No. 2.2e-28;
Matches 101; Conservative 63; Mismatches 125;
13.7%; Score 386.5; DB 32.1%; Pred. No. 1.1e-28; ive 62; Mismatches 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 518
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520 MNAPPISOPVPNRANRELGLDGDDMDIPW---CDLNIKEKIGAGSFGTVHRAEWHGSDVA 576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --IPYHKLADLRYLSRGASGTVSSARHADWR-VQVA 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 821;
                                      APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene and TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                       ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
ADDRESSEE: No. 5367065ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                             COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/928,464
FILING DATE: 19920810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.3%; Score 376; DB 1; Le 30.7%; Pred. No. 3.2e-27; ive 60; Mismatches 111;
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US-08-003-311B-2
Sequence 2, Application US/08003311B
Patent No. 5444166
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19920810
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN-
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32,279
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TOPOLOGY: 1:--
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                                                                                                                                                                                                                                                                                                                  Floppy disk
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Best Local Similarity 30.77
Matches 98; Conservative
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793 WKRPSFATIMDLLRPLIKS
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                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                       COUNTRY: UZIP: 19103
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                                                                                                                                                                                                                                       STATE:
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ASLDNEFVLRLEGVIEKVNWDQDPRPALVTKFMENGSLSGLLQSQCPRP---WPLLCRLL 121
                                                                             186 EGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSV-SQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71 HKARFSYIFPILGICNEPEF----LGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRIL 125
                                                                                                                                                                                                                                       HEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 PTIPYHKLADLRYLSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDVLREAEIL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAP
                                                                                                                                                           GHRPVINEESLPY - - - DIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 ASLDNEFVLRLEGVIEKVNWDQDPKPALVTKFMENGSLSGLLQSQCPRP---WPLLCRLL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTHER INFORMATION: Dominant Negative Mutant Embodiment US-09-329-418-4
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09329418
Patent No. 6096539
GENERAL INFORMATION:
APPLICANT: ZENECA Limited
TITLE OF INTEMPTION:
FILE REFERENCE: PHM. 70536
CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13.4%; Score 380; DB 3; L
ilarity 31.7%; Pred. No. 6.6e-28;
Conservative 62; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
US-07-928-464-2
; Sequence 2, Application US/07928464
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                                                                                                                                                                                                                                                                                          302 FLEAVIQLKKTKLQSVSSA 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       302 FLEAVIQLKKTKLQSVSSA 320
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293 NMNAAVSTVKDFLSOLRSS 311
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Best Local Similarity
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LENGTH: 518
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Matches 101;
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 821;
                 TITLE OF INVENTION: Constitutive Triple Response Gene TITLE OF INVENTION: and Mutations NUMBER OF SEQUENCES: 13
                                                                                                    ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and ADDRESSEE: No. 5444166ris
STREET: One Liberty Place - 46th Floor
CITY: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13.3%; Score 376; DB 1; Lot 30.7%; Pred. No. 3.2e-27; Live 60; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/003,311B
FILING DATE: January 12, 1993
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lori Y. Beardell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-1108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/928,464
FILING DATE: AUGUST 10, 1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-08-261-432-2
; Sequence 2, Application US/08261432
APPLICANT: Kieber, Joseph J. TITLE OF INVENTION: ConstituTITLE OF INVENTION: and Muta
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278 DERPSFLKCLIELEPVLRT 296
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein US-08-003-311B-2
                                                                                     CORRESPONDENCE ADDRESS:
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Best Local Similarity
Matches 98; Conserva
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162 IADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVIT 219
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692 VCDFGLSRLKASTFLSSKSAAGTPE-----WMAPEVLRDEPSNE-----KSDVYSFGVIL 741
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30.7%; Pred. No. 3.2e-27;
ive 60; Mismatches 111; Indels
  Constitutive Triple Response Gene
                                                                                     ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
ADDRESSEE: No. 5602322ris
STREET: One Liberty Place - 46th Floor
GITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,432
FILING DATE: June 17, 1994
                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                             and Mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: June 17, 1994
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/003,311
FILING DATE: January 12, 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Lor1 Y. Beardell
REGISTRATION NUMBER: 34,293
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
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793 WKRPSFATIMDLLRPLIKS 811
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amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 13.3
Best Local Similarity 30.7
Matches 98; Conservative
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; MOLECULE TYPE: protein
US-08-261-432-2
                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                   NUMBER OF SEQUENCES:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                              U.S.A.
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COUNTRY:
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Sequence 5, Application US/09035706
Patent No. 6001622
                                                                                                                                                                                                        FEATURE:
; OTHER INFORMATION: Kinase Domain
US-09-329-418-6
                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                               Best Local Similarity 34.1
Matches 95; Conservative
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MEDIUM TYPE: Diskette
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APPLICATION NUMBER:
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CLASSIFICATION:
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STREET: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           46 VKHL---HIHTPLLDSER-KDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 577 VKILMEQDFH-----AERVNEFLREVAIMKRLRHPNIVLFMGAVTQPPNLSIVTEYLSRG 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 SLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVK 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 WEVLSRKOPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPH--RARMISLIESGWAQNP 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
            Sequence 2, Application PC/TUS9307347
GENERAL INFORMATION:
APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene and TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS: 6
CORRESPONDENCE ADDRESS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.3%; Score 376; DB 5; Length 82 30.7%; Pred. No. 3.2e-27; Live 60; Mismatches 111; Indels
                                                                                                                                                     ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07347
                                                                                                                                                                                    STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UPN-1086
                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/09329418 Patent No. 6096539
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Miller, Suzanne E. REGISTRATION NUMBER: 32,279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: UP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  278 DERPSFLKCLIELEPVLRT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|||| : | |::::
793 WKRPSFATIMDLLRPLIKS 811
                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 821 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 30.7
Matches 98; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 19930805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein PCT-US93-07347-2
                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                       COUNTRY: U
ZIP: 19103
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PCT-US93-07347-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGTIIY 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSV-SQGHRPVIN 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 IFPILGICNEPEF-----LGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGV 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18 LADLRYLSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDVLREAEILHKARFSY 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LENGELVGKGGFGTVFRAQHRKWGYDVAVKIVN-----SKAISREVKAMASLDNEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103;
APPLICANT: ZENECA Limited
TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
FILE REFERENCE: PHM.70536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | || || : | : |: |: |: || : || : || E--LPQAGPETPGLEGLKELMQLCWSSEPKDRPSFQECL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 EESLPY - - - DIPHRARMISLIESGWAQNPDERPSFLKCL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Dedhar, shoukat
APPLICANT: Hannigan, Greg
TITLE OF INVENTION: Integrin-Linked Kinase and
TITLE OF INVENTION: Its Uses
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.1%; Score 372; DB 3; 34.1%; Pred. No. 1.3e-27; ive 53; Mismatches 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Bozicevic & Reed, LLP
285 Hamilton Avenue, Suite 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                             CURRENT APPLICATION NUMBER: US/09/329,418
CURRENT FILING DATE: 1999-06-11
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 261
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11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          188 GTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQG 245
                                                                                                                                                                                                                                                                                                                                                                                                                                      68 EILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHE 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 IALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36; Gaps
                                                                                                                                                                                                                                                                                                                                                                  13 IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHL---HIHTPLLDSER-KDVLREA 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 CKRL-----EIPRNLNPQVAAIIEGCWTNEPWKRPSFATIMDLLRPL 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 HRPVINEESLPYDIPH--RARMISLIESGWAQNPDERPSFLKCLIELEPV 293
                                                                                                                                                                                                                                                                                         Query Match 13.0%; Score 369; DB 3; Length 263; Best Local Similarity 32.4%; Pred. No. 2.6e-27; Matches 94; Conservative 56; Mismatches 104; Indels
REGISTRATION NUMBER: 36,677
REFRENCE/DOCKET NUMBER: KIN-2CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650.327-3400
TELEFRAX: 650 327-3431
TELEFAX:
                                                                                                       INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 263 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear GS-09-035-706-5
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Search completed: June 14, 2001, 08:06:04 Job time: 96 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

June 14, 2001, 08:04:28 ; Search time 13.68 Seconds (without alignments) 1352.190 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-445-223-1 2829 1 MNGEAICSALPTIPYHKLAD......PEILVVSRSPSLNLLQNKSM 540

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

93435 seqs, 34255486 residues Searched:

93435 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	tion) HOU	mus 1	arab	homod	dict	uns i	dict	homod	andn	rattı	homod	arab	caen	homod	homod	pos	mus 1	avia	avian	homod	homod	gallı	cotu	mus r	mus	mus r	homod	drose	dugesia	рошо	avian	рошо	drosophi
	Description		260855	5609	3546	P18160	062073	8161	043318	5202	P16067	002779	7735	7292	0594	P80192	P46197	P28028	0533	9962	P51617	5056	004982	4908	P42682	P43404	P24604	P42680	P11346	P42687	P43403	P23049	P42681	8630
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SUMMARIES		_HUMAN	OUSE	ARATE	UMAN	DICDI	_MOUSE	DICDI	HUMAN	ANGJA	RAT	HUMAN	ARATH	_CAEEL	HUMAN	HUMAN	BOVIN	MOUSE	AVII1	AVEVE	HUMAN	HUMAN	CHICK	COLUM	OUSE	MOUSE	OUSE	UMAN	_DROME	DUGTI	HUMAN	AVIET	HUMAN	DROME
SO	9	ANR3_	RIP_MOUSE	CTR1_ARATH	RIP_HUMAN	KYK1_DICDI	M3K7_	KYK2_DICDI	M3K7_HUMAN	ANPB_ANGJA	ANPB_RAT	M3KA_HUMAN	RLK5_ARATH	KRAF_	ANPB_HUMAN	M3K9_HUMAN	ANPB_BOVIN	KRAB_MOUSE	RMIL_AVII1	RMIL_AVEVR	IRA1_HUMAN	KRAB_HUMAN	RMIL_CHICK	RMIL_COTJA	TXK_MOUSE	ZA70_MOUSE	TEC_MOUSE	TEC_HUMAN	KRAF	SPK1_DUGTI	ZA70_	SEA_A	TXK_H	SRC2_
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	Query Match Length	19.1	13.9	[3,3	13.0	1.1	1.0	10.7	9.0	10.4				0.5							9.8							9.6		9.6			4.	9.5
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	Score	541.5	394	376	369	313.5	311	303.5	300.5	295	292.2	290	289.5	287.5	287.5	284	280.5	277.5	277.5	277.5	277.5	277.5	277.5	277.5	273.5	273	272.5	272.5	272	271.5	27(268.5	265.5	261
	Result No.	-	2	m	4	S	9	7	ω,	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

P46573 arabidopsis	024585 zea mays (m	Q62406 mus musculu	P13368 drosophila	P24062 rattus norv	P35991 mus musculu	. 008680 rattus norv	P43298 arabidopsis	Q03146 mus musculu	P54755 gallus gall	P15208 mus musculu	Q9syq8 arabidopsis
APKB_ARATH	CRI4_MAIZE	IRA1_MOUSE	7LES DROME	IG1R_RAT	BTK_MOUSE	EPA3_RAT	TMK1_ARATH	DDR1_MOUSE	EPA5_CHICK	INSR_MOUSE	CLV1_ARATH
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'n	259	254	51.5	251	50.5	249	248.5	247.5	247.5	347.5	247
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ALIGNMENTS

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MGD; MGI:108212; Ripkl.
InterPro; IPR000488; -.
InterPro; IPR000719; -.
InterPro; IPR002290; -.
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Pfam; PF00069; pkinase;
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                                                                                                                                     23;
                                                                                                                                                                                                 84 ICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLL 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SQLDSGVSQAVEGPEELSR 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 SSSE--SKLPSSGSGKRLS-GVS------SVS--SVDSAFSSRGSLSLS 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
SERINE/THREONINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN
                                                                                                                                                         83
                                                                                                                                                                             86
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MEDLINE-95277838; PubMed-7538908;
Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;
"RIP: a novel protein containing a death domain that interacts with Pas/APO-1 (CD95) in yeast and causes cell death.";
                                                                                                                                                                                                            GASGIVSSARHADWRVQVAVK---HLHIHTPLLDSERKDVLREAEILHKARFSYIFPILG
                                                                                                                                                                     1 GFGQOYKVRHVHWKTWLAIKCSPSLHVD----DRERMELLEEAKKMEMAKFRILLPVYG
                                                                                                                                                                                                                                                     QKSRA-SIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVINEEŞLPYDIP
                                                                                                                                                                                                                                                                                               HRAR----MISLIESGWAQNPDERPSF-------LKCLIELEPVLRTFEEITFL
                                                                                                                                                                                                                                                                                                                                         250 ARPRACSHLIRLMQRCWQGDPRVRPTFQGNGLNGELIRQVLAALLPVTGRWRSPGEGFRL
                                                                                                                                                                                                                                                                                                                                                                                |: :: | |: | |: | ESEVIIRVTCPLSSPQEITSETEDLCEKPDDEVKETAHDLDVKSPPEPRS-----E
                                                                                                                                                                                                                                                                                                                                                                                                             356 GSPETSRSLPAPQ-DNDF-LSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHKTTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                       414 CSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTEACLNQSLDALLSRDLIMKED
                                                                                                                                                                                                                                          144 HHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEG--GTIIYMPPENYEPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474 YELVSTKPTRTSKVRQLLDTTDIQGEEFAKVIVQKLKDNKQMGLQPYPEILVVSRSPSL
                                                                                                                                     Indels 113;
                                                                                                                  Length 832;
                                                                              SIMILAKITI.
5D8FFFD5F04F7ECB CRC64;
                                                                                                                 19.1%; Score 541.5; DB 1; 31.7%; Pred. No. 2.9e-30;
                                                                                                                                      77; Mismatches 178;
                                                     SIMILARITY)
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P (BY SIMILA)
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                                                                                                                           Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
                                                                                                                  Query Match
Best Local Simi
Matches 171;
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Q60855;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82
1 81:513-523(1995).
FUNCTION: INTERACTS WITH THE DEATH DOMAIN OF FAS AND TRADD AND FUNITATES APOPTOSIS. IT IS RECRUITED BY TRADD TO THERI IN A THEDEPENDENT PROCESS. REQUIRED FOR THERI ACTIVATION OF NF-KAPPA B. TISSUE SPECIFICITY: FOUND AT LOW LEVELS IN ALL TISSUES. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LHHDLKTQNILLDNEFHVKIADFGLSKWRMMS-LSQSRSSKSAP-----EGGTIIYM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 VINE--ESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEP-VLRTFEEITFLEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       249 NVEEILEYCPREI-----ISLMERCWQAIPEDRPTFLGIEEEFRPFYLSHFEEYV-EED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIIIEEGNYSLVMEYMEKGNLMHVL--KTQI-DVPLSLKGRIIVEAIEGMCYLHD--KGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PPE----NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 VIQLKK-----TKLQSVSSAIHLC------DKKKMELSLNIPVNHGPQEESCGSSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      351 LHENSGSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 394; DB 1; Length 656;
Pred. No. 4e-20;
6; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transferase; Serine/threonine-protein kinase; ATP-binding;
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ABB350B523879933 CRC64;
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ATP (BY SIMILARITY)
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            :99
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31.0%;
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138
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                                                                                                                                                                                                                                           STRAIN=CV. COLUMNIA, TISSUE-Seedling, MEDLINE-93161417; PubMed-8431946; Kieber J.J., Rothenberg M., Roman G., Feldmann K.A., Ecker J.R.; CTR1, a negative regulator of the ethylene response pathway in Arabidopsis, encodes a member of the raf family of protein kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- TISSUE SPECIFICITY: EXPRESSED IN BOTH SEEDLINGS AND ADULT PLANTS.
-!- MISCELLANEOUS: CTR1 MUTANTS DISPLAY ETHYLENE-TREATED PHENOTYPES,
RESULTING IN PLANTS WITH SWALL, UNEXPANDED LEAVES AND WHOSE SEED
COTYLEDON GROWTH IS IMPAIRED.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MIL/RAF SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                         Bevan M., Pohl T., Weizenegger T., Bancroft I., Mewes H.-W., Rudd S.
Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: ACTS AS A NEGATIVE REGULATOR IN THE ETHYLENE RESPONSE
                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Sukaryota; Viridplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D->E: IN CTR1-1; EXHIBITS ETHYLENE-
TREATED PHENOTYPE.
2922D3DCDOCC15BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
E->K: IN CTR1-4; EXHIBITS ETHYLENE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P11362; IRUL.
InterPro; IPR000719; -
InterPro; IPR002290; -
Pfam; PF00069; Pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS500119; PROTEIN_KINASE_DOM; 1.
Transferase; Setine/threonine-protein kinase; ATP-binding.
                                                          01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
SERINE/THREONINE-PROTEIN KINASE CTR1 (EC 2.7.1.37).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                             821 AA.
                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L08790; AAA32780.1; -. EMBL; AL162506; CAB82938.1; -.
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                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               565
                                                                                                                                                                                                                                                                                                                             Cell 72:427-441(1993).
                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           821 AA;
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PATHWAY
                           CTR1_ARATH
Q05609;
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MUTAGEÑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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NP_BIND
BINDING
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CTR1_ARATH
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                                                                                                                                                        101
                                                                                                                                                                                                                                   631
                                                                                                                                                                                                                                                                                                                 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    692 VCDFGLSRLKASTFLSSKSAAGTPE-----WMAPEVLRDEPSNE------KSDVYSFGVIL 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIP_HUMAN STANDARD; PRT; 671 AA.
013546; 013180;
01-NOV-1997 (Rel. 35, Created)
01-NOV-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
SERINE/THREDNINE PROTEIN KINASE RIP (EC 2.7.1.-) (CELL DEATH PROTEIN RIP) (RECEPTOR INTERACTING PROTEIN).
RIPKI OR RIP.
    45
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MEDLINE=95277838; PubMed=7538908;
Stanger B.Z., Leder P., Lee T.-H., Kim E., Seed B.;
"RIP: a novel protein containing a death domain that interacts with TesARPO-1 (CD95) in yeast and causes cell death.";
Cell 81:513-523(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- FUNCTION: INTERACTS WITH THE DEATH DOMAIN OF FAS AND TRADD AND INITIATES APOPTOSIS. IT IS RECRUITED BY TRADD TO THERI IN A THF-DEPENDENT PROCESS. REQUIRED FOR THERI ACTIVATION OF NF-KAPPA B. -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
    --IPYHKLADLRYLSRGASGTVSSARHADWR-VQVA
                                                                              520 MNAPPISQPVPNRANRELGLDGDDMDIPW---CDLNIKEKIGAGSFGTVHRAEWHGSDVA
                                                                                                                                                                                                          SLNELLHRKTE:YPDVAWPLRFRILHEIALGVNYLHNWTPPLLHHDLKTQNILLDNEFHVK
                                                                                                                                                                                                                                                                                                                                                       || || || || SLYRLLHKSGAREQLDERRRLSAMAYDVAKGMNYLHNRNPPIVHRDLKSPNLLVDKKYTVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WEVLSRKOPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPH--RARMISLIESGWAQNP
                                                                                                                                                        VKHL---HIHTPLLDSER-KDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVIT
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MEDLINE=96200892; PubMed=8612133;
Hsu H., Huang J., Shu H.-B., Baichwal V.R., Goeddel D.V.;
"TNF-dependent recruitment of the protein kinase RIP to the TNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Butel
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Immunity 4:387-396(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            278 DERPSFLKCLIELEPVLRT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           793 WKRPSFATIMDLLRPLIKS 811
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MNGEAICSALPT
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EMBL; U50062; AAC32232.1; -.

12;

Gaps

50;

13.3%; Score 376; DB 1; Length 821; 30.7%; Pred. No. 9.6e-19; Live 60; Mismatches 111; Indels

Conservative

Query Match Best Local Similarity Matches 98; Conserv

us-09-445-223-1.rsp

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ACT_SITE
CONFLICT
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NP_BIND
BINDING
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Matches
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                                                                                                                                                                                                                                         12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                303 SLKKEYSNENAVVKRMOSLOLDCVAVPSSRSNSATEQPGSLHSSQGLGMGPVEESWFAPS 362
                                                                                                                                                                                                                                                                                                  GICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPL 142
                                                                                                                                                                                                                                                                                                                                      LHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPE-----GGTIIYMP 194
                                                                                                                                                                                                                                                                                                                                                 INE -- ESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTFEEITFLEAVI 307
                                                                                                                                                                                                                                                                                                                                                                                                                                 249 VDDITEYCPREI----ISLMKLCWEANPEARPTFPGIEEKFRPFYLSQLEESVEEDVK 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1990 (Rel. 16, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).
PROTEIN SPLA OR DPYKI.
                                                                                                                                                                                                                                                            LSRGASGTVSSARHADWRVQ-VAVKHLHIHTPLLDSERKDVLREAEILHKARFSYIFPIL 82
                                                                                                                                                                                                                                                                              LDSGGFGKVSLCFH---RTQGLMIMKTVYKGPNCIEHNEALLEEAKMMNRLRHSRVVKLL 79
                                                                                                                                                                                                                                                                                                                                                                                      64;
                                                                                                                                                                                                                     / Match 13.0%; Score 369; DB 1; Length 671; Local Similarity 28.8%; Pred. No. 2.2e-18; nes 112; Conservative 67; Mismatches 146; Indels
                                                                         PROSITE; PS00108; PROTEIN_KINASE_JCM; 1.
PROSITE; PS50011; PROTEIN_KINASE_JCM; 1.
PROSITE; PS50017; DEMUH_DOMAIN; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                      POLY-ARG.
T -> S (IN REF. 3).
BADC4E7E70456ABE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
NCBI_TaxID=44689;
                                                                                                                        PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1584 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          351 LHENSGSPETSRSLPAPQDNDFLSRKAQD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEH-----PQEENEPSLQSKLQD 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-JH10;
MEDLINE-97053827; PubMed-8898241;
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M
                        InterPro; IPR000488; -.
InterPro; IPR00019; -.
InterPro; IPR002290; -.
Pfam; PF00531; death; 1
Pfam; PF0069; pkinase; 1.
U25994; AAC50137.1;
P11362; 1FGI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                           671 AA;
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SEQUENCE FROM N.A.
                    MIM; 603453;
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P18160;
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DOMAIN
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BINDING
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT DEVELOPMENT WITH A PEAK DURING THE MOUND STAGE OF MORPHOGENESIS.
-i- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES BUT ALSO TO SERINE/THREONINE PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          olls G.H., Osherov N., Loomis W.F., Spudich J.A.;
Dictyostellum dual-specificity kinase splA is essential for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55;
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                                                                                                                                                                                                        "Developmentally regulated protein-tyrosine kinase genes in Dictyostellum discoideum.";
Mol. Cell. Biol. 10:3578-3583(1990).
-!- FUNCTION: ESSENTIAL FOR SPORE DIFFERENTIATION.
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN TYROSINE TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D -> R (IN REF. 2).
V -> L (IN REF. 2).
MW; 5D1589458D8E01E3 CRC64;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                               SEQUENCE OF 1248-1584 FROM N.A.
MEDLINE-90287147; PubMed-1972546;
Tan J.L., Spudich J.A.;
                                                                           Development 122:3295-3305(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U32174; AAB41125.1; -. EMBL; M33785; AAA33202.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; A35670; A35670.

PIRSP, P1362; IFOT.

DictyDb; D003010; DykA.

InterPro; IPR000107;

InterPro; IPR000119;

InterPro; IPR001660;

InterPro; IPR001660;

Pfam; PF00356;

Pfam; PF00562; SRM; 1.

Pfam; PF00652; SRM; 3.
                                                        spore differentiation
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10;

64227 MW; 97C8F6F3C8E283EE CRC64;

579 AA;

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                              1341 KLRHPNVVQFLGACTAGGEDHHCIVTEWMGGGSLRQFLTDHFNLLEQNPHIRLKLALDIA 1400
                                                                                                     1455
                                                                                                                                                       130 LGVNYLHNMTPPLLHHDLKTQNILLDN------EFHVKIADFGLSKWRMMSLS 176
                                                                                                                                   QSRSSKSAPEGGIIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPL 236
                                                                                                                                                                                                   QIMY-SVSQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLR 295
72 KARFSYIFPILGICNE--PEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIANCE FROM N.A.

MEDIANE-96123277; PubMed-8533096;

Yamaquchi K., Shirakabe K., Shibuya H., Irie K., Ohishi I., Ueno N.,

Taniquchi T., Nishida E., Matsumcto K.;

Identification of a member of the MAPKKK family as a potential

mediator of TGF-bera signal transduction.";

Science 270:2008-2011(1995).

-I-FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE YET UNDEFINED MAPKKS.

MEDIATOR OF TGF-BETA SIGNAL TRANSDUCTION. STIMULATES NF-KAPPA B
                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE KINASE KINASE SUBFAMILY.
-!- SIMILARITY: IN THE C-TERMINAL SECTION; STRONG, TO C210RF7.
                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (Rel. 40, Last Sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
MITOGEN-ACTIVATED PROTEIN KINASE KINASE 7 (EC 2.7.1...)
(TRANSFORMING GROWTH FACTOR-BETA-ACTIVATED KINASE 1) (TGF-BETA-ACTIVATED KINASE 1).
MAP3K7 OR TAK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transferase; Serine/threonine-protein kinase; ATP-binding. DOMAIN 8 16 POLY_SER.
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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----TFKQIIVHLKEMEDQGVSS 1569
                                                                                                                                                                                                                                                                      296 TFEEITFLEAVIQLKKTKLQSVSS 319
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MGD; MGI:1346877; Map3k7.
InterPro; IPR000719; -.
                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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63
156
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Q62073;
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BINDING
ACT_SITE
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M3K7_MOUSE
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                                                                                                                                                                          83 RVNHPNIVKLYGACLNP--VCLVMEYAEGGSLYNVLHGAEPLPYYTAAHAMSWCL---- 135
                                                                                                                                                                                                                                                                                                                                                       243 SQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTF----E 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                           297 PLOYPCOYSDEGOSNSATSTGSFMDIASTNTSNKSDTNMEGVPATNDTIKRLESKLLKNQ 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      414 QDLTVTGTEPGOVSSRSSSPSVRMITTSGPTSEKPARSHPWTPDDSTDTNGSDNSIPMAY 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 KARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYP-----DVAWPLRFRIL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 WDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGNSERLQPGIAQQWIQSKREDIVNQMTE 453
                                                                    13 IPYHKLADLRYLSRGASGTVSSARHADWRVQ-VAVKHLHIHTPLLDSERKDVLREAEILH 71
                                                                                                     31 IDYKEIEVEEVVGRGAFGVVCKAK---WRAKDVAIKQIE----SESERKAFIVELRQLS 82
                                                                                                                                                                                                                                                                                                         126 HEIALGVNYLHNMTP-PLLHHDEKTQNILL-DNEFHVKIADFGLSKWRMMSLSQSRSSKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       454 ACLNQSLD------ALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIQGEEF
                                                                                                                                                                                                                                                                                 184 APEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNP-LQIMYSV
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                                    100;
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MEDLINE=90287147; PubMed=1972546;
Tan J.L., Spudich J.A.;
"Developmentally regulated protein-tyrosine kinase genes in
Length 579;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mol. Cell. Biol. 10:3578-3583(1990).
-!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBL_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES SERINE/THREONINE PROTEIN KINASES.
                                   Conservative 97; Mismatches 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             538
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11.0%; Score 311; DB 1; 23.5%; Pred. No. 2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     524 VAELDQDEKDQQNTSRLVQEHKKLLDENKSLSTYYQQCK
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Mol. Cell. Biol. 10:3578-3583(1990)
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Query Match
Best Local Similarity
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P18161;
                                 Matches 136;
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         the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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                                                                                                                                                                                                                                                                                                                                                                                                          GVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGTI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                            77 YIFPILGICNEPEFLGIVTEYMPNGSLNELLHR-----KTEYPDVAWPLRFRILHEIAL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 I---YMPPENYEPGOKSRASIKHDIYSYAVITWEVLSRKQPFEDV---TNPLQIMYSVSQ 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 CNPRWRPPELTK--NLGHYSEKVDVYCFSLVVWEILTGEIPFSDLDGSQRSAQVAYA--- 325
                                                                                                                                                                                                                                                                                                                                                                 43; Gaps
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                                                                                                                                                                 Pfan: PF00069; pkinase; 1.
PROSITE: PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sakurai H., Shigemori N., Hasegawa K., Sugita T.;
"TGF-beta-activated kinase 1 stimulates NF-kappa B activation by
NF-kappa B-inducing kinase-independent mechanism.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M3K7_HUMAN STANDARD; PRT; 606 AA.
043317; 043319;
01-07-2000 (Rel. 40, Crasted)
01-07-2000 (Rel. 40, Last sequence update)
01-07-2000 (Rel. 40, Last annotation update)
MITOGEN-ACTIVATED PROTEIN KINASE KINASE 7 (EC 2.7.1.-)
MITOGEN-ACTIVATED ROWTH FACTOR-BETA-ACTIVATED KINASE 1) (TGF-BETA-ACTIVATED KINASE 1)
                                                                                                                                                                                                                                                                                                                                         Length 410;
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and the
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                                                                                                                                                                                                                                               PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                       10.7%; Score 303.5; DB 1; llarity 30.1%; Pred. No. 4.2e-14; Conservative 57; Mismatches 102;
the Swiss Institute of Bioinformatics
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                                                               or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                      BY
                                                                                                                                                                                                                                                                                                    Ψ.,
                                                                                        EMBL; M33784; AAA33203.1; -.
                                                                                                                                                                                                                                                                                                    46386
                                                                                                                  HSSP; P11362; 1FGI.
DictyDb; DD03011; pykB.
InterPro; IPR000719; -.
InterPro; IPR001245; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                      PIR; B35670; B35670.
                                                                                                                                                                                                                                                             114
135
232
410 AA;
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISOFORM 1C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 SQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRTF----E 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----TFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNIPVNH 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      72 KARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYP-----DVAWPLRFRIL 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 HEIALGVNYLHNMTP-PLLHHDLKTQNILL-DNEFHVKIADFGLSKWRMMSLSQSRSSKS 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357 AKQQSESGRLSLGASRGS--SVESLPPTSEGKRMSADMSEIEARIAATTAYSKPKRGHRK 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 IPYHKLADLRYLSRGASGTVSSARHADWRVQ-VAVKHLHIHTPLLDSERKDVLREAEILH 71
chem. Biophys. Res. Commun. 243:545-549(1998).
FUNCTION: CAN PHOSPHORYLATE AND ACTIVATE YET UNDEFINED MAPKKS.
MEDIATOR OF TGF-BETA SIGNAL TRANSDUCTION. STIMULATES NF-KAPPA B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVATION.
-:- ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1A, 1B (SHOWN HERE) AND 1C;
PRODUCED BY ALTERNATIVE SPLICING.
-:- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
MAP KINASE KINASE KIDRAE SUBFAMILY.
-:- SIMILARITY: IN THE C-TERMINAL SECTION; STRONG, TO C21ORF7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         184 APEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNP-LQIMYSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_AT; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NI)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
MISSING (IN ISOFORM 1A).
PLAAPCPUNKE -> ARTSCRIEGG (I
MISSING (IN ISOFORM IC).
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ATP (BY SIMILARI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.6%; Score 300.5;
22.8%; Pred. No. 1.2e
:ive 96; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB009357; BAA25026.1; -. EMBL; AB009356; BAA25025.1; -. EMBL; AB009358; BAA25027.2; -.
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Pfam; PF00069; pkinase; 1.
PROSITE; PS00107; PROTEIN_
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DOMAIN

B 14

DOMAIN

36

291

NP_BIND

BINDING

63

63

ACT_STTE

156

VARSPLIC

VARSPLIC

519

606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000719;
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156
404
509
519
606 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         602614;
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SEQUENCE
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STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                           460
481
1050
790
                                                                                                                                                                                                                                                                     Receptor; Transmembran cGMP synthesis; Signal
                                            rPR001828;
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366 36
415 41
1050 AA;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P55202;
01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-2000 (Rel. 40, Last annotation update)
ATRIAL NATRIUMETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B)
(GUANTIATE CYCLASE) (EC 4.6.1.2) (NPR-B) (ATRIAL NATRIUMETIC PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MISCELLANBOUS: THERE SEEM TO BE AT LEAST THREE AND RECEPTORS: TWO WITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANGE OF AND FROM THE CIRCULATION WITHOUT A ROLE IN SIGNAL TRANSDUCTION.
SIMILARITY: SOME SIMILARITY WITH CONSERVED REGION OF CATALYTIC
                                                                                                                                                                                                                                                                                                       SERLQPGIAQQWIQSKREDIVNQMTEACLNQSLD------ALLSRDLIMKEDYE 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anguilla japonica (Japanese eel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterygii, Neopterygii, Teleostei, Anguilliformes, Anguilloidei;
Anguillidae, Anguilla.
380 -CYFMKLHHCP----GNHS-----WDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGN 427
                                                                                                                                                                            475 PTRSHPWTPDDSTDTNGSDNSIPWAYLTLDHQLQPLAPCPNSKESMAVFEQHCKMAQEYM 534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPATION WITH TESTING AND THE TOTAL PEPTING TECEPOIL B GING COMPATION WITH TESTING WITH THE TESTING THE TESTING THE TECEPOIL B GING THE TESTING WITH THE OFFICE THE CUNCTION: RECEPTOR FOR NARRIURETIC PEPTINES. HAS GUANYLATE CYCLASE ACTIVITY ON BINDING TO LIGAND. THE ORDER OF POTENCY OF LIGANDS IN STIMULATING GC ACTIVITY IS CNP > VNP > ANP.

-!- CATALYTIC ACTIVITY: GTP = 3,'5'-CYCLIC GMP + PYROPHOSPHATE.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- TISSUE SPECIFICITY: HIGH LEYELS FOUND IN LIVER, ATRIUM AND GILL. MODERATE LEVELS FOUND IN BRAIN AND VENTRICLE, AND LOW LEVELS IN GESOPHAREAL, SPHINTER, STOMACH, POSTERIOR INVESTINE AND KIDNEY.
-!- INDUCTION: BY OSBOSIS: LEVELS BECREASE UNDER SALINE CONDITIONS: TWO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: TO ANP-A ON THE COMPLETE SEQUENCE, AND TO ANP-C IN THE EXTRACELLULAR AND TRANSMEMBRANE DOMAINS.
                                                                                                                                                                                                                                                    476 LVSTKPTRISKVRQLLDTTDIQGEEFAKVIVQKLKD--NKQMGLQPYPEILVVSRSPSLN
                                            Hirose S.; "Cloning and expression of eel natriuretic peptide receptor B and \ensuremath{\text{and}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Katafuchi T., Takashima A., Kashiwagi M., Hagiwara H., Takei Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1050 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94298823; PubMed=7913035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN OF PROTEIN KINASES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                     534 LLQNK 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                        585 YQQCK 589
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ID ANPB_ANGJA
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267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 DVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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01-APR-1990 (Rel. 14, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-F (GUANYLATE CYCLASE) (EC 4.6.1.2) (NPR-B) (ATRIAL NATRIURETIC PEPTIDE
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15 YHKLADLRYL--SRGAS-GTVSSARHADWRV------QVAVKHLHIHTPLLDSERK 61
                                                                                                                                                                                                                                            B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 FRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      625 YSLINDIVKGMNFLHNSYIG-SHGNLKSSNCVVDSRFVLKITDYGLASFRSSCENEDSHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            511 YHKCAGSRLTISQRGSSYGSLITA-HGKYQLFAKTGYFKGNLVAIK--HVNKKRIELTRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   684 LYAKKLWTAPE--LLIYDRHPPQGTQKG------DVYSFGIILQEIALRNGPFYVDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --SRSSKSAPEGGTIIY--MPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                            ATRIAL NATRIURETIC PEPTIDE RECEPTOR
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(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL)
                                         PRINTS; PROCO25; NATURE CYCLASES_1; 1.
PROSITE; PSO0452; GUANYLATE_CYCLASES_1; 1.
PROSITE; PSO015; GUANYLATE_CYCLASES_2; 1.
PROSITE; PSO011; PROFIELN_KIRASE_DOM; 1.
Receptor; Transmembrane; Glycoprotein; Phosphorylation; Lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1050;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW; F3AC6DDD17BD3832 CRC64;
                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC...) (
                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                             INTERCHAIN (PROBABLE)
INTERCHAIN (PROBABLE)
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BY SIMILARITY.
BY SIMILARITY.
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Pfam; PF01094; ANF_receptor; 1.
Pfam; PF00069; pkinase; 1.
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Best Local Similarity 29.09
Matches 87; Conservative
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DYLREAEILHKARFSYIFPILGICNEPEFLGIYTEYMPNGSLNELLHRKTEYPDVAWPLR 121

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                                                                                                         SIMILARITY: TO ANP-A ON THE COMPLETE SEQUENCE, AND TO ANP-C IN TH
                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AȚRIAL NATRIURETIC PEPTIDE RECEPTOR B. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
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                    Schulz S., Singh S., Bellet R.A., Singh G., Tubb D.J., Chin H., Garbers D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00458; ANF_RECEPTORS; 1.
PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
PROSITE; PS50125; GUANYLATE_CYCLASES_2; 1.
PROSITE; PS5011; PROTEIN_KINASE_DOM; 1.
RECEPTOR; Transmembrane; Glycoprotein; Phosphorylation; Lyase; GGMP synthesis; Signal.
                                                                      cyclase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5062C49228CC14A3 CRC64;
                                                                 "The primary structure of a plasma membrane guanylate c
demonstrates diversity within this new receptor family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL). PROTEIN KINASE LIKE. BY SIMILARITY.
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INTERCHAIN (PROBABLE).
N-LINKED (GLCNAC...) (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR AND TRANSMEMBRANE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
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MEDLINE-89376566; PubMed-2570641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01094; ANF_receptor; 1. Pfam; PF00069; pkinase; 1. PRINTS; PR00255; NATPEPTIDER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M26896; AAA41205.1; -.
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IPR001054; -.
IPR001170; -.
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1047 AA;
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TRANSMEM
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                                                                                                                                                                                                                           182 KSAPEGGTIIY-----MPPE----NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPF--E 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             281 PSFLKCLIELEPVLRTFEE---ITFLE-AVIQLKK-----TKLQSVSSAIHLCDKKKMEL 331
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621 YSLINDLVKGMAFLHNSIIS-SHGSLKSSNCVVDSRFVLKIIDDYGLASFR-----S
                                                                                                                                                                                                                                                                     728 GLDLSPKEIVQKVRNGQRPYFRPSIDRTQLNEE------LVLLMERCWAQDPTER
                                                                                           122 FRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSS
                                                                                                                                                                                                                                                                                                                                                              DV-TNPLQIMYSVSQGHRPV-----INEESLPYDIPHRARMISLIESGWAQNPDER
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BELINE-96128179; PubMed-8536694;

BOTOW D.S., Devereux L., Tu G.F., Price G., Nicholl J.K.,
Sutherland G.R., Simpson R.J.;
"Complete nucleotide sequence, expression, and chromosomal localisation of human mixed-lineage kinase 2.";

Eur. J. Blochem. 234:492-500(1995).
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"Cloning and characterization of MST, a novel (putative)
serine/threonine kinase with SH3 domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              M3KA_HUMAN STANDARD; PRT; 954 AA.
01279; 012761; 014871;
01-FEB-1994 (Rel. 28, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last sequence update)
MITOGEN-ACTIVATED PROTEIN KINASE KINASE ID (MIXED LINEAGE KINASE 2) (PROTEIN KINASE MST).
MAP3KIO OR MLK2 OR MST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95249256; PubMed=7731697;
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MEDLINE=93238756; Pubmed=8477742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 244-480 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 SLNIPVNHGPQEE 344
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                        564
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21;

Indels 77; Gaps

Length 1047;

15 YHKLADLRY-LS-RGAS-GTVSSARHADWRV------QVAVKHLHIHTPLLDSERK 61

10.3%; Score 292.5; DB 1; 1larity 27.3%; Pred. No. 8.8e-13; Conservative 80; Mismatches 114;

Similarity

Query Match Best Local Simi Matches 102;

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SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A
                                                                                                                       RLK5_ARATH
P47735;
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                                                                                                            RLK5_ARATH
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                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                    Serine/threonine-protein kinase; Tyrosine-protein kinase; SH3 domain.
                                                                                                                                                                                                                                                                                                                                                                      -> AQAAGRRQPHQPALWL (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::| |:||||| | |::| |||: ||| | |---QVARGMNYLHNDAPVPIIHRDLKSINILILEAIENHNLADTVLKITDFGLAREWH-- 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DALAVAYGVA-----MNKLTLPIPSTCPEPFARLLEECWDPDPHGRPDFGSILKRLEVI 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQSALFQMPLESFHSLQEDWKLEIQHMFDDLRTKEKELRSREEELLRAAQEQRFQEEQLR 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVA--WPLRFR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ILHEIALGVNYLHNMTP-PLLHHDLKTQNILLDN--EFH-----VKIADFGLSK-WRMM 173
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLFGALOHPNIIALRGACLNPPHLCLVMEYARGGALSRVLAGRRVPPHVLVNWAV--- 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 RREQELAEREMDIVERELHIL---MCQLSQEKP------RVRKRKGNFKRSRL 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                          13 IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHLHIHTPLLDSER-----KDVLR 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLSQSRSSKSAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 NPLQIMYSVSQGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----QLKKTKLQSVSSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQLHENSGSPETSRS
                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches 174; Indels 144;
                                                                                                                                                                                                                                                                                       BY SIMILARITY.
LEUCINE-ZIPPER (BY SIMILARITY).
LEUCINE-ZIPPER (BY SIMILARITY).
ARC/LYS-RICH (BASIC).
SRL -> AV (IN REF. 2).
G -> S (IN REF. 2).
V -> A (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                    10.3%; Score 290; DB 1; Length 954; 23.7%; Pred. No. 1.2e-12;
                                                                                                                                                                                                                                                                                                                                                                                     538F4AAA559B0ABA CRC64;
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                                                                                                                                                                                                                                                             PROTEIN KINASE.
                                                                                                                                     Pfam, PF00069; pkinase; 1.
PRINTS; PR00109; TYRKINASE.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS001017; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                         POLY-GLU.
                                                                                                                                                                                                                                                                                                                                                                               REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                      78;
                                     EMBL; X90846; CAA62351.1; -...
EMBL; Z48615; CAA88531.1; -...
PIR; S32468; S32468.
HSSP; P00523; 2PTK.
MIM; 600137; -...
                                                                                                                                                                                                                                                                                                                                                                                        103623
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                    InterPro; IPR000719; -. InterPro; IPR001245; -.
                                                                                                           IPR001452; -. IPR002965; -.
                                                                                                                            Pfam; PF00018; SH3; 1.
Pfam; PF00069; pkinase
                                                                                                                                                                                                                                                                                                                                                                                        954 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                      Transferase;
                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Sim
Matches 123;
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NP_BIND
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                                                                                                            InterPro;
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STALL LANDERS
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                                                                                                                                                                                                                             Horn M.A., Walker J.C.;
"Blochemical properties of the autophosphorylation of RLK5, a receptor-like protein kinase from Arabidopsis thaliana.";
Blochim. Blophys. Acta 1208:65-74(1994).
-i- COFACTOR: HAVE SIGNIFICANTLY GREATER ACTIVITY IN THE PRESENCE OF MN2+ THAN MG2+.
Antonolu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C., Swaby L.K., O'Shaugnessy A., Vil D., Shekher M., Matero A., Shah R., Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A., Chen E., Marra M., Martienssen R., McCombie W.R., Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                          -i- PTM: AUTOPHOSPHORYLATED ON SERINE AND THREONINE RESIDUES.
-i- SIMILARITY: TO PROTEIN KINASES IN THE C-TERMINUS. BUT DOES NOT SEEM TO HAVE CONSERVED A KINASE ACTIVITY.
-i- SIMILARITY: CONTAINS 18 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam: PF00560; LRR; 14.
Pfam: PF00069; McInase; 1.
PRINTS; PR00019; LEURICHRPT.
PROSITE; PS00107; PROTEIN.KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN.KINASE_ST; 1.
PROSITE; PS50011, PROTEIN.KINASE_DOM; 1.
Transferase; Serine/theonine-protein kinase; ATP-binding; Transmembrane; Glycoprotein; Phosphorylation; Leucine-rich repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RECEPTOR-LIKE PROTEIN KINASE 5. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                            -! - TISSUE SPECIFICITY: EXPRESSED IN ROOTS AND ROSETTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
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LRR
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LRR
                                                                                                                                                                                         CHARACTERIZATION.
MEDLINE-94368830; PubMed-8086440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRR CLRR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AL021749; CAA16889.1; -. EMBL; AL161572; CAB79651.1; -. HSSP; P00523; 2PTK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M84660; AAA32859.1; -.
                                                                                                                                                   Nature 402:769-777(1999).
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SIGNAL
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DOMAIN
TRANSMEM
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLH--RKTEYPDVAWPLRF 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RILHEIALGVNYL-HNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 KSAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYS 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                        16 HKLADL----RYLSRGASGTVSSARHADWRVQVAVKHLHIHTP-----LLDSERKDVL- 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- FUNCTION: PROTEIN KINASE THAT PARTICIPATES IN THE INDUCTION OF C.ELEGANS VULVA. ACTS DOWNSTREAM OF THE RAS PROTEIN LET-60.
-i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MIL/RAF SUBPAMILY.
-i- SIMILARITY: CONTAINS 1 ZINC-DEPENDENT PHORBOL-ESTER AND DAG BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-93247635; Pubmed-8483497;
MEDLINE-93247635. Pubmed-8483497;
MEDLINE-93247635; Pubmed-8483497;
"C. clegans lin-45 raf gene participates in let-60 ras-stimulated vulval differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          242 VSQ----GHRPVINEESLPYDIPHRARMISLIESG---WAQNPDERPSFLKCLIELEPV
                      (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                             31;
    (POTENTIAL)
                                                                                                                                                                                                                  K->E: LOSS OF CATALYTIC ACTIVITY.
                                                                                                                                                                                                                                                                                                  Length 999;
                                                                                                                                                                                                                                                                                                                                             Indels
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01-0CT-2000 (Rel. 40, Last annotation update)
RAF HOMOLOG SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-).
                                                                                                                                                                                                                                       F5793D899EA0C6A7 CRC64;
N-LINKED (GLCNAC...
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                               Mismatches 123;
                                                                                                                                                                                                                                                                                                    10.2%; Score 289.5; DB 1
32.3%; Pred. No. 1.3e-12;
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                                                                                                                                                                                                                                         109095 MW;
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                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vulval differentiation."
Nature 363:133-140(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caenorhabditis elegans.
                                                                                                                                                                                                                                       999 AA;
                                                                                                                                                                                                                                                                                                                           Similarity
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    1150
210
2210
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2282
2452
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7111
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Q07292;
                                                                                                                                                                                                                                                                                                                                             97;
                                                                                                                                                                                                                                                                                                    Query Match
Best Local Si
Matches 97;
                        CARBOHYD
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BINDING
ACT_SITE
MUTAGEN
SEQUENCE
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PIR; S05514; S05514.
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EMBL;
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  14;
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P20594; Q9UQ50; 060871;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
ATRIAL NATRIURETIC PEPTIDE RECEPTOR B PRECURSOR (ANP-B) (ANPRB) (GC-B) (GUANTLATE CYCLASE) (EC 4.6.1.2) (NPR-B) (ATRIAL NATRIURETIC PEPTIDE B-TYPE RECORDS).
NPR2 OR ANPRB.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                             466 POKPHHE--DWEILPNEFIIOYKVGSGSFGTVYRGEFFGTVAIKKLNVVDP-TPSQMAAF 522
                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                              PTIPYHKLADLRYLS-----RGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDV 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chang M.S., Lowe D.G., Lewis M., Hellmiss R., Chen E., Goeddel D.V.;
                                                                                                                                                                                                                                                                                                                                                  580 IDILKQVSLGMNYLHSKN--IIHRDLKTNNIFLMDDMSTVKIGDFGLATVKTKWTVNGGQ
                                                                                                                                                                                                                                                                                                                                                                            QSRSSKSAPEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPL
                                                                                                                                                                                                                                                                                                  64 LREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLR--
                                                                                                                                                                                                                                                                                                                                        122 FRILHEIALGVNYLHNMTPPLLHHDLKTQNI-LLDNEFHVKIADFGL----SKWRMMSLS
                                                                                                                                                                                                                                                                                                                                                                                                                  237 QIMYSVSQGH-RPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                Transferase; Serine/threonine-protein kinase; ATP-binding; Zinc;
                                                                                                                                                                                                                                              45;
                                                                                                                                                                                                                           DB 1; Length 813;
                                                                                                                                                PHORBOL-ESTER AND DAG BINDING.
                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                     BY SIMILARITY.
6376E968C6859E49 CRC64;
                                                                                                                                                         PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                         Score 287.5; DB 1;
Pred. No. 1.4e-12;
65; Mismatches 127;
                                                                              PROSITE; PSO00479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PS50081; DAG_PE_BIND_DOM_2; 1.
PROSITE; PS500101; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DAM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GEVLERLRDIILPKLTRSQSAPNVLHL 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 TFEEITFLEAVIQLKKTKLQSVSSAIHL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (LONG ISOFORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Brain;
MEDLINE=89365195; PubMed=2570358;
                PIR; S33261; S33261.
HSSP; P1362; 1AGW.
InterPro; IPR000219; -.
InterPro; IPR002219; -.
InterPro; IPR002290; -.
Pfam; PF00130; DAG_PE-bind; 1.
                                                                                                                                                                                               90491 MW;
                                                                                                                                                                                                                          10.2%;
27.7%;
       AAA28142.1;
                                                                                                                                                                                                                                           91; Conservative
                                                                          pkinase;
                                                                                                                                         binding.
                                                                                                                                                                                              813 AA;
                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                        Pfam; PF00069;
         L15347;
                                                                                                                                        Phorbol-ester
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAURDITEL M.;

TOGMP-dependent and independent inhibition of a K+ conductance by a "cGMP-dependent and independent inhibition of a K+ conductance by natriuretic peptides. Molecular and functional studies in human proximal tubule cells.";

Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.

CYCLASE ACTIVITY ON BINDING OF ANF. SEEMS TO BE STIMULATED MORE CYCLASE ACTIVITY BY BRAIN NATRIURETIC PEPTIDE. HAS GUANYLATE CYCLASE ACTIVITY ON BINDING OF ANF. SEEMS TO BE STIMULATED MORE CYCLASE ACTIVITY: GTP = 3, 15, -CYCLIC GMP + PYROPHOSPHATE.

CHARLYTIC ACTIVITY: GTP = 3, 15, -CYCLIC GMP + PYROPHOSPHATE.

CHARLYTIC ACTIVITY: GTP = 3, 15, -CYCLIC GMP + PYROPHOSPHATE.

SHORT FORM/NPR-BI; ARE PRODUCED BY ALITERNATIVE SPLICING.

HITH GUANYLATE CYCLASE ACTIVITY (ANP-A AND ANP-B) AND ONE (ANP-C) WHICH IS PROBABLY RESPONSIBLE FOR THE CLEARANCE OF ANP FROM THE CLEARANCE OF ANP FROM THE CLEARANCE OF ANP FROM THE CHECKLAND WITHOUT A ROLE IN SIGNAL TRANSDUCTION.

CHARLANTING SIMILARITY WITH CONSERVED REGION OF CATALYTIC DUMAIN OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - SIMILARITY: TO ANP-A ON THE COMPLETE SEQUENCE, AND TO ANP-C IN TH
                                                                                                                                                                                                                        Rehemudula D., Nakayama T., Soma M., Takahashi Y., Uwabo J., Sato M., Izumi Y., Kamatsuse K., Ozawa Y.; "Structure of the type B human matriuretic peptide receptor gene and association of a novel microsatellite polymorphism with essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO ADENYLYL CYCLASE CLASS-4/GUANYLYL CYCLASE
                                                of
two different receptor guanylate cyclases."; haure 341:68-72(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mollerup S.,
Schlatter E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Kidney;
Hirsch J.R., Meyer M., Magert H.J., Forssmann W.G., Mollerup
Herter P., Weber G., Cermak R., Ankorina-Stark I., Schlatter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXTRACELLULAR AND TRANSMEMBRANE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (SHORT ISOFORM).
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                                                                                                                                                 SEQUENCE FROM N.A. (LONG ISOFORM)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 DVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77; Gaps
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INTERCHAIN (PROBABLE).

INTERCHAIN (PROBABLE).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                         ATRIAL NATRIURETIC PEPTIDE RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                               PRINTS; PRO0255; NATPEPTIDER.
PROSTTE; PS00458; ANE RECEPTORS; 1..
PROSITE; PS00452; GUANYLATE_CYCLASES_1; 1.
PROSITE; PS500125; GUANYLATE_CYCLASES_2; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSTTE; PS50011; PROTEIN_AINASE_DOM; 1.
PROSTOR: Jansmembrane; Glycoprotein; Phosphorylation; Lyase; CGMP synthesis; Signal, Alternative splicing.
SIGNAL
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817FB74D6B31F7EF CRC64;
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PROTEIN KINASE LIKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15 YHKLADLRY-LS-RGAS-GTVSSARHADWRV-----
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                                                                                                                   InterPro; IPR001828; -. Pfam; PF01094; ANF_receptor; 1. Pfam; PF00069; pkinase; 1.
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1047 AA; 117021
                                       InterPro; IPR000719; -.
                                                                                                   InterPro; IPR001170; -.
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RESULT

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21;
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Transferase; Serine/threonine-protein kinase; Tyrosine-protein kinase;
ATP-binding.
1 1 PROTEIN KINASE.
DOMAIN 3 271 PROTEIN KINASE.
NP_BIND
BINDING 30 17 APP ....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139 VENGDLSNKI-LKITDFGLAREWH------RTTKMS-AAGTYAWMAPEVIRASMFSKGS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LMEDCWNPDPHSRPSFTNILDQLTTIEESGFFEMPKDSFHCLQDNWKHEIQEMFDQLRAK 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPVLRTFEEITFLEAVIQLKKTKLQSVSSAIHLCDKKKMELS------LNIPVNHG 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43 QVAVKHLHIHTPLLDSER---KDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPN 100
                                                                        01-OCT-2000 (Rel. 40, Last annotation update)
MITGGEN-ACTIVATED PROTEIN KINASE KINASE 9 (EC 2.7.1.-) (MIXED
LINEAGE NINASE 1) (FRAGMENT).
MAP3K9 OR MIKI OR PRKEI
                                                                                                                                                                                                                                                                                       101 GSLNELLHRKTEYPD--VAWPLRFRILHEIALGVNYLHN-MTPPLLHHDLKTQNIL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----LDNEFHVKIADFGLSK-WRMMSLSOSRSSKSAPEGGTIIYMPPENYEPGQKSRAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            208 IKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVINEESLPYDIPHRARMIS
                                                                                                                                                  Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.0%; Score 284; DB 1; Length 394; 26.4%; Pred. No. 9.1e-13; Live 62; Mismatches 125; Indels 122;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY).
LEUCINE-ZIPPER (BY SIMILARITY).
LEUCINE-ZIPPER (BY SIMILARITY).
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DBE40B7D31047FD8 CRC64;
   394 AA
                                                          Last sequence update)
   PRT;
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MEDLINE-93238756; PubMed-8477742;
                                      28, Created)
28, Last seq
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   STANDARD;
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PIR; JU0229; JU0229.
HSSP; P11362; 1FGI.
MIM; 600136; -.
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                                  01-FEB-1994 (Rel. 01-FEB-1994 (Rel.
                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                     NCBI_TaxID=9606;
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M3K9_HUMAN
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350	394	391	
300 EKELRTWEEELTRAALQQKNQE-ELLRRREGELAEREIDILERELNIIIHQL 350	341 PQEESCGSSQLHENSGSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSW 394	351 CQEKPRVKKRKGKFRKSRLAQPVLPFPHGHSRCPGGTGSSW 391	
qq	Qγ	QQ	

Search completed: June 14, 2001, 08:04:51 Job time: 23 sec

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OM protein - protein search, using sw model

June 14, 2001, 08:04:28; Search time 53.04 Seconds Run on:

(without alignments)
699.668 Million cell updates/sec

US-09-445-223-1 2829 Title: Perfect score:

1 MNGEAICSALPTIPYHKLAD......PEILVVSRSPSLNLLQNKSM 540 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters:

198801 seqs, 68722935 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_67:* Database :

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	receptor interacti			serine/threonine p	probable serine/th	probable serine/th	protein kinase ATN	probable protein k	protein kinase hom	probable mitogen-a	protein kinase 6 (hypothetical prote	protein-tyrosine k	transforming growt		₽	transforming growt	serine/threonine p	dual leucine zippe	hypothetical prote	protein-tyrosine k	protein kinase hom	. MAP3K delta-1 prot	transforming growt			natriuretic-peptid	protein kinase (EC	atrial natriuretic
SUMMARIES	ID	I49299	T07406	T48400	T09479	T09911	T00726	T46150	T06576	T05137	T52626	S29851	T02584	T18276	JC5955	T04683	T12955	JC5957	A55318	JC5399	T45697	B35670	T01451	T48544	JC5956	T01182	T05675	S45636	JC2363	OYRTBR
	DB	5	7	7	7	~	7	7	7	~	7	7	7	7	7	'n	7	7	7	7	~	~	7	~	7	7	7	7	7	
	Length	656	829	821	671	963	1015	370	982	736	406	462	116	1584	579	553	475	267	888	888	784	410	390	988	909	443	545	1050	668	1047
ф	Query Match	13.9	13.6	13.3	13.0	12.7	12.7	12.3			11.6	11.2	11.2	11.1	11.0	10.9	10.8	10.8	10.8	10.8	10.8	10.7	10.7	10.7	10.6			10.4	10.3	10.3
	Score	394	385.5	376	369	359.5	359	348.5	340	335.5	327.5	317.5	316.5	313.5	312	307	306.5	306.5	306.5	306.5	305	303.5	302.5	301.5	300.5	0	297.5	59	292.5	292.5
	Result No.		7	Э	7	5	9	7	æ	6	10	11	12	13	14	15	16	17	18	19	20		. 22	23	24	25	56	27	28	29

protein-tyrosine k	hypothetical prote	mixed-lineage prot	receptor-like prot	receptor-like prot	hypothetical prote	receptor-like prot	serine/threonine-s	protein kinase lin	natriuretic peptid	serine/threonine-s	receptor-like prot	hypothetical prote	mixed-lineage prot	ser/thr specific p	ser/thr specific p
								•							
T18287	T45684	868178	S27756	T48499	T10665	T45692	T02731	533261	OYHUBR	T10664	T45690	T01134	JU0229	T50811	T51791
~	7	Н	-	7	7	7	7	-	Н	7	7	7	7	7	7
1338	816	954	666	1192	855	871	884	813	1047	959	819	694	394	356	402
10.3	10.3	10.3	10.2	10.2	10.2	10.2	10.2	10.2	10.2	10.1	10.1	10.1	10.0	10.0	10.0
292	290.5	290	289.5	289.5	289	288.5	288	287.5	287.5	287	286	285.5	284	283	283
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT

C;Accession: I49299
R;Stanger, B.Z.; Leder, P.; Lee, T.H.; Kim, E.; Seed, B.
A;Tille: R.IP: a novel protein containing a death domain that interacts with Fas/APO-1
A;Reference number: A56913; MUID:95277838 C;Species: Mus musculus (house mouse) C;Date: 09-Mar:1996 #sequence_revision 09-Mar-1996 #text_change 05-Nov-1999 A.Accession: 149299
A.Status: preliminary
A.Molecule 'type: mRNA
A.Residues: 1-656 <RES>
A.Cross-references: EMBL:UZ5995; NID:g829618; PIDN:AAB60487.1; PID:g829619
C.Genetics:
C.Genetics:
C.Superfamily: protein kinase homology
F;15-293/Domain: protein kinase homology receptor interacting protein RIP - mouse

19; 83 GICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPL 142 | | | : | | | | : | | | : | | | : | | | | : | | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 143 LHHDLKTQNILLDNEFHVKIADFGLSKWRMMS-LSQSRSSKSAP-----EGGTIIYM 193 194 PPE----NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRP 248 249 VINE -- ESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEP-VLRTFEEITFLEA 305 306 VIQLKK-----TKLQSVSSAIHLC-----DKKKMELSLNIPVNHGPQEESCGSSQ 350 302 VASLKKEYPDOSPVLORMFSLOHDCVPLPPSRSNSEQPGSLHSSGGLOMGPVEESWFSS- 360 249 NVEELLEYCPREI-----ISLMERCWQAIPEDRPTFLGIEBEFRPFYLSHFEETV-EED 301 351 LHENSGSPETSRSLPAPQDNDFLSRKAQDCYFMKLHHCPGNHSWDSTISGSQRAAFCDHK 410 361 -----SPE-----YPQDENDRSVQA-----KLQEEASYHAF------GIFAEKQ 393 23 LDSGGFGKVSLCYHRSHGFVILKK---VYTGPNRAEYNEVLLEEGKMMHRLRHSRVVKLL 79 24 LSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDV-LREAEILHKARFSYIFPIL 82 82; 13.9%; Score 394; DB 2; Length 656; 31.0%; Pred. No. 1.1e-15; 66; Mismatches 144; Indels Best Local Similarity 31.0% Matches 131; Conservative Query Match δ δλ qq ŏ g à g g g g ă δý Qγ

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A;ritie: RIP: a novel protein containing a death domain that interacts with Fas/APO-1
A;Reference number: A56913; MUID:95277838
A;Accession: 138992
                                                                                                                                                                                                                 A map position: 5 A map position: 5 A map position: 5 A mintrons: 216/3; 317/2; 364/3; 399/2; 468/1; 560/1; 573/3; 596/3; 630/2; 658/3; 691/3; 671/215.150 C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom C; Keywords: ATP F; 549-812/Domain: protein kinase homology <KIN>F; 554-812/Domain: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #text_change 17-Nov-2000
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A;Molecule type: mRNA
A;Residues: 300-513,'S',515-671 <RES>
A;Cross-references: EMBL:UZ5994; NID:g829616; PIDN:AAC50137.1; PID:g829617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     46 VKHL---HIHTPLLDSER-KDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNG 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 821;
A,Accession: A45178
A,Status: preliminary, not compared with conceptual translation
A,NoLecule type: DNA
A,Residues: 1-468,470-821 <KIE>
A,Note: sequence extracted from NCBI backbone (NCBIP:124878)
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.3%; Score 376; DB 2; Length 82: 30.7%; Pred. No. 1.6e-14; tive 60; Mismatches 111; Indels
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A;Molecule type: mRNA
A;Residues: 1.671 < HUDA.
A;Cross-references: EMBL:U50062; NID:g3426026; PID:g3426027
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C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: T09479; I38992
R;Huang, J.; Hsu, H.; Baichwal, V.R.; Goeddel, I
submitted to the EMBL Data Library, August 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: ATP binding; phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   278 DERPSFLKCLIELEPVLRT 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ristanger, B.Z.; Leder, P.; Lee,
Cell 81, 513-523, 1995
A;Title: RIP: a novel protein con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 30.79
Matches 98; Conservative
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A; Accession: T09479
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A; Residues: 1-629 «WANA
A; Residues: 1-629 «WANA
A; Cross-references: EMBL:Y13273; NID:e1050452; PIDN:CAA73722.1; PID:e334294
A; Experimental source: strain UC82B; sub_species Mill
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Υ.
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C; Species: Arabidopsis thallana (mouse-ear cress)
C; Species: Arabidopsis thallana (mouse-ear cress)
C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 17-Nov-2000
C; Accession: T48400; A45178
R; Bevan, M.; Pohl, T.; Walzenegger, T.; Bancroft, I.; Mewes, H.W.; Rudd, S.; Lemcke, submitted to the Protein Sequence Database, March 2000
A; Reference number: 224492
A; Accession: T48400
A; Atacus: preliminary
A; Molecule type: DNA
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A; Molecule type: DNA
A; Residues: 1-821 < BEV>
A; Cross-references: EMBL:ALI62506
A; Experimental source: cultivar Columbia; BAC clone F17C15
R; Kleber, J.J.: Rothenberg, M.; Roman, G.; Feldmann, K.A.; Ecker, J.R.
Cell 72, 427-441, 1993
A; Title: CTR1, a negative regulator of the ethylene response pathway in Arabidopsis,
A; Reference number: A45178; MUID:93161417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                                      C.Species: Lycopersicon esculentum (tomato)
C.Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50 --HIHTPLLDSERKDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELL 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted to the EMBL Data Library, May 1997
A:Reference number: 216016
A:Accession: TOT406
A:Status: prellminary; translated from GB/EMBL/DDBJ
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33.2%;
                                                                                                                                                                                                                                                                       - tomato
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Matches 104; Conservative
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                                                                                                                                                                                                                                                                   probable protein kinase
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           411 TTP 413
                                                                                 394 TKP 396
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Best Local 3
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Submitted to the EMBL Data Library, April 1998
A;Description: Genomic sequence for Arabidopsis thaliana BAC F22013.
A;Reference number: 214200
A;Accession: 100726
A;Accession: 100726
A;Accession: Lranslated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1015 <SHID
A;Cross-references: EMBL:AC003981; NID:g3063438; PID:g3063459; GSPDB:GN00059; ATSP:F2
A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: cultivar Columbia; BAC clone T3A5
R;Quetier, F.; Rieger, M.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Zipp, M.; Salan
submitted to the Protein Sequence Database, May 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Map position: 1
A:Introns: 71/3; 219/3; 360/3; 395/2; 760/1; 773/3; 796/3; 830/2; 856/3; 889/3; 912/3
C;Keywords: phosphotransferase; protein kinase
                                                                                                                                                             probable serine/threonine-specific protein kinase (EC 2.7.1.-) F22013.21 - Arabidopsi C; Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
C;Accession: T00726
R;Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.; eologis, A.; Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEILHKARFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILH, 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 IPYHKLADLRYLSRGASGTVSSARHADWR-VQVAVKHLHIHTPLLDSE-----RKDVLRE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 QGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1015;
                         QCHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.7%; Score 359; DB 2;
llarity 32.9%; Pred. No. 2.1e-13;
Conservative 53; Mismatches 105.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
es 96; Conserv
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-370 < BLO>
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Best Local S:
Matches 96,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable serine/threonine-specific protein kinase (EC 2.7.1.-) T22A6.310 - Arabidopsis C.Species: Arabidopsis thallana (mouse-ear cress)
C.Species: Arabidopsis thallana (mouse-ear cress)
C.Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Oct-1999
C.Accession: T09911
R.Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Ma submitted to the Protein Sequence Database, June 1999
A.Reference number: 216896
A.Accession: T09911
                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
                                                                                                                                                                                                                                                                 195 PE----NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPV 249
                                                                                                                                                                                                                                                                                                                                                                                                         307
                                                                                                                                                                                                                                                                                                                                                                                                                            :| | :|: : |:| ||||| || || ||| || ||: :: |||| ||: : ELHIKERVGAGSFGTVHRAEWHGSDVAVKILSIQ-DFHDDQFREFLREVCKQAVAIMKRV 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 GICNEPEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPL 142
                                                                                                                                                                                        303 SLKKEYSNENAVVKRMOSLOLDCVAVPSSRSNSATEQPGSLHSSOGLGMGPVEESWFAPS 362
                                                                                                                                                                                                                                            143 LHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPE-----GGTIIYMP 194
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                                              Gaps
                                                                                   82
                                                                                                          23 LDSGGFGKVSLCFH---RTQGLMIMKTVYKGPNCIEHNEALLEEAKMMNRLRHSRVVKLL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLRYLSRGASGTVSSARHADWR-VQVAVKHLHIHTPLLDSERKDVLRE----AEILHKA 73
                                                                                                                                                                                                                                                                                                                                                 RFSYIFPILGICNEPEFLGIVTEYMPNGSLNELLHRKT -- EYPDVAWPLRFRI -- -- - LH
                                                                               24 LSRGASGIVSSARHADWRVQ-VAVKHLHIHTPLLDSERKDVLREAEILHKARFSYIFPIL
                                                                                                                                                                                                                                                                                                                                                                                                       250 INE--ESLPYDIPHRARMISLIESGWAONPDERPSFLKCLIELEPVLRTFEEITFLEAVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---SSAIHLCDKKKMELSLNIPVNHGPQEESCGSSQ
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                                         64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-963 <BEV>
A; Residues: 1-963 <BEV>
A; Cross-references: EMBL:AL078637; GSPDB:GN00062; ATSP:T22A6.310
A; Experimental source: cultivar Columbia; BAC clone T22A6
C; Genetics:
Length 671;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12.7%; Score 359.5; DB 2; 31.7%; Pred. No. 1.8e-13; ive 60; Mismatches 105;
                                       67; Mismatches 146;
  ; DB 2;
3.3e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :Introns: 286/3; 386/2; 434/3; 473/2; 543/1; 6
Keywords: phosphotransferase; protein kinase
  Score 369;
Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----PQEENEPSLOSKLQD 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                351 LHENSGSPETSRSLPAPQDNDFLSRKAQD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OLKK-----TKLOSV----
13.0%;
28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 31.78
Matches 93; Conservative
                                     Matches 112; Conservative
                       Similarity
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A;Map position: 4
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                    Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
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C;Accession: T52626
R;Jouannic, S.; Hamal; A.; Leprince, A.S.; Tregear, J.W.; Kreis, M.; Henry, Y.
Gene 229, 171-81, 1999
A;Title: Characterisation of novel plant genes encoding MEKK/STE11 and RAF-related pr A;Reference number: 224447; MUID:99196996
A;Accession: T52626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Introns: 116/2; 260/3; 302/3; 477/1; 490/3; 513/3; 547/2; 573/3; 606/3; 629/3; 646/
A:Note: F7H19.240
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A)Molecule type: mRNA
A)Residues: 1406 <JOUD>
A)CLOSS-references: EMBL:Y14199; NID:q2253009; PIDN:CAA74591.1; PID:q2253010
A)Experimental source: cultivar Columbia
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cyaccession: T05137 Cyducactering of the property of the prope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein kinase homolog F7H19.240 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable mitogen-activated protein kinase MAP3K delta-1 [imported] - Arabido
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 08-Dec-2000
                                                       EIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPE 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 -RFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSR 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               238 IMYSVSQGHRPVINEESLPYDIPH--RARMISLIESGWAQNPDERPSFLKCLIELEPVLR 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 674 VVGVVGFMDRRL-----DLPEGLNPRIASIIQDCWQTDPAKRPSFEELISQMMSLFR 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSKSAPEGGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQ 237
                                                                                              GGTIIYMPPE--NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVS-
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                                                                                                                                                                                                                                                                                                                                                           244 QGHRPVINEESLPYDIPHRARMISLIESGWAQNPDERPSFLKCLIELEPVLR 295
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Best Local Similarity 32.>.
The conservative 79, Conservative
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A;Reference number: 216409
A;Accession: T08394
A;Accession: T08394
A;Accession: T08394
A;Accession: T08394
A;Accession: T08394
A;Accession: T08394
A;Residues: 1-370 <QUE>
A;Cross references: EMBL:AL049862; GSPDB:GN00061; ATSP:F18B3.10
A;Experimental source: cultivar Columbia; BAC clone F18B3
C;Genetics: ATSP:F18B3.10
A;Genetics: ATSP:F18B3.10
A;Genetics: ATSP:F18B3.10
A;Genetics: ATSP:F18B3.10
A;Genetics: ATSP:F18B3.10
A;Genetics: ATSP:F18B3.10
A;Genetics: ATSP:F1B3.10
A;Genetics: ATSP:F1B3.
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A,Experimental source: cultivar Ailsa craig
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable protein kinase TCTR2 - tomato
C;Species: Lycopersicon esculentum (tomato)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C;Accession: T06576
R;Hackett, R.M.
submitted to the EMBL Data Library, March 1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 VAVKHLHIHT--PLLDSERKDVLREAEILHKARFSYIFPILGICNEPEFLGIVTEYMPNG 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SLNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEF-HV 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIADFGLSKWRMMSLSQSRSSKSAPEGGTIIYMPPENYEP----GQKSRASIKHDIYSY 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPDERPSFLKCLIELEPVLRTFEEITFLEAVIQLKKTKLQSVSSAIHLCDKKKMELSLNI 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -----RMSSDSS-----IGTTL 312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.3%; Score 348.5; DB 2 29.2%; Pred. No. 2.4e-13;
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A,Accession: T06576
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-982 <HAC>
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Matches 94; Conserva
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protein-tyrosine kinase (EC 2.7.1.112) 1 - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Nov-2000
C;Accession: T18276, A35670
R;Nuckolls, G.H.; Osherov, N.; Loomis, W.F.; Spúdich, J.A.
Bevelopment 122, 3295-3305, 1996
A;Title: The Dictyostelium dual-specificity kinase splA is essential for spore differ A;Reference number: 218852; MUID:97053827
A;Accession: T18276
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-1584 <NUC>
A;Cross-references: EMBL:U32174; NID:9974333; PID:9974334; PIDN:AAB41125.1
R;Tab, J.L.; Spudich, J.A.
Nol. Cell. Biol. 10, 3578-3583, 1990
A;Title: Developmentally regulated protein-tyrosine kinase genes in Dictyostelium dis
                                                                                     hypothetical protein T16B24.18 - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 17-Mar-2000
C; Accession: T02S84
R; Rounsley, S:D: Kaul, S:; Lin, X:; Retchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke submitted to the EMBL Data Library, August 1998
A; Description: Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence.
A; Reference number: 214679
A; Accession: T02S84
A; Residues: translated from GB/EMBL/DDBJ
A; Residues: 1-776 CROU>
A; Residues: 1-776 CROU>
A; Cross-references: EMBL: ACCO4697; NID: 93402671; PID: 93402686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 2
A;Note: T16B24.18
C;Superfamily: S-receptor kinase; protein kinase homology; S-locus-specific glycoprot
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A;Residues: 'R',1249-1434,'L',1436-1584 <TAN>
A;Cross-references: GB:M33785; NID:g167775; PIDN:AAA33202.1; PID:g167776
A;Note: the authors translated the codon TAT for residue 271519 as Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 HKLADLRYLSRGASGTVSSARHADWRVQVAVKHLHIHTPLLDSERKDVLREAEILHKARF
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C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homold C;Keywords: ATP: phosphotransferase F:154-419/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein kinase 6 (EC 2.7.1.-) - soybean
C;Species: Glycine max (soybean)
C;Species: Glycine max (soybean)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C;Accession: S29851; S27760
R;Feng, X.H.; Zhao, Y.; Bottino, P.J.; Kung, S.
Biochlim. Blophys. Acts 1172, 200-204, 1993
A;Title: Cloning and characterization of a novel member of protein kinase family from shacesion: S29851; MUID:93176812
A;Accession: S29851
A;Molecule type: mRNA
A;Residues: 1-462 <FENS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 YLHNMTPPLLHHDLKTQNILLDNEFHVKIADFGLSKWRMMSLSQSRSSKSAPEGGTIIYM 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPE--NYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNPLQIMYSVSQGHRPVIN 251
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              Length 406;
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                                                                                                   Indels
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11.6%; Score 327.5; DB.2; 32.1%; Pred. No. 4.5e-12; ive 50; Mismatches 107;
                                                                                              Conservative
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A; Introns: 47/3; 72/2
Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C; Superfamily: unassigned ser/Thr or Tyr-specific protein kinase
C; Reywords: ATP: phosphotransferase; tyrosine-specific protein kinase
F; 1287-1566/Domain: protein kinase homology «Kin»
F; 1285-1303/Region: protein kinase ATP-binding motif
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R. Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.
B. Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.
B. Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.
B. Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.
B. Sakurai, H.; Shigemori, N.; Hasegawa, K.; Sugita, T.
A. Reference number: JC5955; MUID:98153801
A. Reference number: JC5955; MUID:98153801
A. Reference number: JC5955
A. Status: preliminary
A. Molecule type: DNA
A. Molecule type: DNA
A. Residues: J-579 cSAKA
A. Residues: J-579 cSAKA
A. Cross-references: DDBJ:AB009356; NID:9224623; PIDN:BAA25025.1; PID:92924624
C.; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
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                                                                                                                                                                                                                                                                           Species: Homo sapiens (man)
Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                      KARFSYIFPILGICNE--PEFLGIVTEYMPNGSLNELLHRKTEYPDVAWPLRFRILHEIA 129
                                                                                                                                                                                                                                                                                                                      130 LGVNYLHNMTPPLLHHDLKTQNILLDN------EFHVKIADFGLSKWRMMSLS 176
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                                                                                                                      11.1%; Score 313.5; DB 2; 28.1%; Pred. No. 1.5e-10; Live 59; Mismatches 119;
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Best Local Similarity 23.58
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Introns: 69/2; 107/3; 176/2; 194/3; 231/3; 289/2; 325/2; 350/1; 408/3; 440/3; 467/3
Note: F8D20.290
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C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: T04683
R.Bevan, M.: Rose, M.: Hempel, S.; Entian, K.D.; Jesse, T.; Heijnen, L.: Vos, P. submitted to the Protein Sequence Database, July 1998
A.Reference number: 215381
A.Rocession: T04683
A.Rocession: T0488
A.Rocession: T0488
A.Rocession: T053 ABEV>
A.Residues: 1-53 ABEV>
A.Coss-references: BMBL:AL031135
A.Experimental source: cultivar Columbia; BAC clone F8D20
C.Genetics:
A.Map position: 4
A.Introns: 69/2: 107/3: 176/2: 194/3: 231/3: 289/2: 325/2: 350/1: 408/3: 440/3:
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                                            ----GSAAWMAPEVFE---GSNYSEKCDVFSWGIILWEVITRRKPFDEIGGPAFRIMWAV
                                                                                                                                                                                                                                                                                                                                           297 PLOYPCOYSDEGOSNSATSTGSFMDIASTNTSNKSDTNMEOVPATNDTIKRLESKLLKNO
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APEGGTIIYMPPENYEPGQKSRASIKHDIYSYAVITWEVLSRKQPFEDVTNP-LQIMYSV
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larity 29.0%; Pred. No. 1e-10;
Conservative 59; Mismatches 112; Indels
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1135764 Sequence I from patent
108789 Arabidopsis thaliana ne
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168123 Sequence 16 from patent
105062 Homo sapiens RIP protei
1 AR044139 Sequence 31 from patent
1 AR305913 Arabidopsis thaliana
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1 AF078330 Homo sapiens receptor
1 AF02844 Homo sapiens SARD-con
1 AF027706 Homo sapiens serine/t
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! AF117829 Homo sapiens 8q21.3
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AB001872 Homo sapiens mRNA for
AF199466 Drosophila melanogast
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! AC004697 Arabidopsis thalian
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Database length: -1216004940
Search time (sec): 2258.700000
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OM Of: US-09-445-223-1 to:
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Query: US-09-445-223-1
Query length: 540
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                                                                                                             About: Results were
                                                        Date: Jun 13, 2001
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D49785 Rattus norvegicus mf
U32174 Dictyostelium discoi
ABO09356 Homo sapiens mkNA
AJ005282 Homo sapiens mRNA
L13436 Homo sapiens guanyla
                                                                                                                                                                                                                                                                                       1 (bases 1 to 2098)
Boldin, M. and Wallach, D.
MODULATORS OF INTRACELLULAR INFLAMMATION, CELL DEATH AND CELL
SURVIVAL PATHWAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   260 ATGAACGGGGAGGCCATCTGCAGCGCCCTGCCACTCCCTACCACAA 309
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Percent Identity: 100.000
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BOLDIN MARK (IL); WALLACH DAVID (IL)
Location/Qualifiers
   8.3e-15
1.5e-14
7.3e-15
1.1e-14
1.3e-14
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                                                                                                                                                            Sequence 2 from Patent W09855507.
A82777 GI:6732464
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1 452 c 449 g 539
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1459
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134 yrLeuHisAsnMetThrProProLeuLeuHisHisAspLeuLysThrGln 150
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                                                                                                                                                                                                                                                                                                                                                                                                                          217 lileThrTrpGluValLeuSerArgLysGlnProPheGluAspValThrA 234
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                                                                                  AsnileLeuLeuAspAsnGluPheHisValLysileAlaAspPheGlyLe
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                                         660 ACCTGCACAATATGACTCCTCTTTACTTCATGACTTGAAGACTCAG
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                                                                                                                                                                     uSerLysTrpArgMetMetSerLeuSerGlnSerArgSerSerLysSerA
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1 (bases 1 to 1623)
McCarthy,J.V., Ni,J. and Dixit,V.M.
RIP2 is a novel NR-kappaB-activating and cell death-inducing kinase 98307936
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TPVNHGPGESCGSQCHENSGSPETSRSLPAPQDNDFLSRRAQDCYFMKLHHCPGNH
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2 (RIP2) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/function="induces cell death"
//note="RIP2; serine/threonine kinase homolog;
//ARD motif"
                                                                                                                                                          517
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                                                                                                                                     pLeuIleMetLysGluAspTyrGluLeuValSerThrLysProThrArgT
                                                                                                                                                                                                                    hrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluGlu
                                                                                                                                                                                                                                                                                                  PhealaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGlyLe
                                                                                                                                                                                                                                                                                                                           uGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsnL
                                                        MetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAs
seq_documentation_block:
LOCUS AF078530 1623 bp mRNA PR
DEFINITION Homo sapiens receptor interacting protein
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Submitted (15-70L-1998) Molecular On Way, South San Francisco, CA 94080, Location/Qualifiers
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/organism="Homo sapiens"
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/gene="RIP2"
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AF078530.1
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VERSION
KEYWORDS
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AUTHORS
TITLE
JOURNAL
MEDLINE
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AUTHORS
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234		267 rLeulleGluSerGlyTrpalaGlnA 	284 euLysCysLeuIleGluLeuGluPro		301 ThrPheLeuGluAlaVailleGinLe 	317 1SerSerAlaIleHisLeuCysAspL 	334 snlleProvalAsnHisGlyProGln	351 LeuHisGluAsnSerGlySerProGl 	384 ysLeuhishisCysProGlyAsnHis 	. 401 SerGlnArgAlaAlaPheCysAspHi 	417 allelleAsnProLeuSerThrAlaG 	434 lyllealaglndlnrpileglnSer 		467 pLeuIleMetLysGluAspTyrGluL 	484 hrSerLysvalargGlnLeuLeuAsp 	501 PhealarysvalilevalGlnLysLe 	517 uGlnProfyrProGlulleLeuValV. 	534 euLeuGlnAsnLysSerMet 540
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351	LeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPr 	367 1100
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. 401	SerGlnargalaalaPheCysAspHisLysThrThrProCysSerSerAl 	417 1250
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484	hrSeriysvalArgGlnLeuLeuAspThrThrAspIleGlnGlyGluGlu 	500 1500
501	PhealalysvalilevalginiysLeulysAspasniysGinMetGlyLe 	517 1550
517 1551	UGINPrOTyrProGlulleLeuValValSerArgSerProSerLeuAsnL 	534 1600

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234
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                                                                                                                                                                                                                                                                                                                                                                 Thome, M., Hofmann, K., Burns, K., Martinon, F., Bodmer, J.-L., Mattmann, C. and Tschopp, J. Identification of CARDIAK, a RIP-like kinase that associates with
                                                                                                                  seq_documentation_block:
LOCUS AF064824 1902 bp mRNA PRI 07-JUL-1998
DEFINITION Homo sapiens CARD-containing ICE associated kinase mRNA, complete
                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-MAY-1998) Institute of Biochemistry, University of Lausanne, Chemin des Boveresses, 155, Epalinges, CH 1066, Switzerland
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Gaps: 0
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2 (bases 1 to 1902)
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1. .1902
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                                 1601 TACTTCAAAATAAAAGCATG 1620
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AF064824.1 GI:3290171
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REFERENCE
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1 MetAsnGlyGluAlaIleCysSerAlaLeuProThrIleProTyrHisLy 17

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267 rLeuileGluSerGlyTrpAlaGlnAsnProAspGluArgProSerPheL 284
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34
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us-09-445-223-1.p2n.rge

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                                                                                                                                                 Pathlogy, Comprehensive Cancer & 1500 E. Medical Center Dr, Ann Arbor,
RICK, a novel protein kinase containing a caspase recruitment domain, interacts with CLARP and regulates CD95-mediated apoptosis 98241596
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225. 1847
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                                                                                         Tobases 1 to 2501)
Inohara,N., Koseki,T., Chen,S., del Peso,L. and Nunez,G. Direct Submission
Submitted (01-0CT-1997) Dept. Pathlogy, Comprehensive Cai
Geriatrics Center, 4-131 CGGC 1500 E. Medical Center Dr, MI 48109, USA
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Gaps: 0
Percent Identity: 99.815
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens serine/threonine kinase RICK (RICK) mRNA, complete
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Inohara,N., del Peso,L., Koseki,T., Chen,S. and Nunez,G.
                                                                                                                                                                                                                                                                                                                                        1143 ACTTTTCTTGAAGCTGTTATTCAGCTAAAGAAAACAAAGTTACAGAGTGT 1192
                                                                                                                                                                                                                                   1293 CTCCATGAAATAGTGGTTCTCCTGAAACTTCAAGGTCCCTGCCAGCTCC 1342
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leCysAsnGluProGluPheLeuGlyIleValThrGluTyrMetProAsn 100
                                                                                                                                    aTrpProLeuArgPheArgIleLeuHisGluIleAlaLeuGlyValAsnT 134
                                                       475 TTTGCAATGAGCCTGAATTTTTGGGAATAGTTACTGAATACATGCCAAAT 524
                                                                                        101 GlySerLeuAsnGluLeuLeuHisArgLysThrGluTyrProAspValAl 117
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 ( bases 1 to 11655)
Ozersky, P., Holmes, A. and Broy, M.
The sequence of Homo sapiens BAC clone CTA-437L15
Unpublished
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Park Avenue, St. Louis, Missouri 63108,
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Park Avenue, St. Louis, Missouri 63108,
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complete sequence.
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AC004003
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Submitted (15-JAN-1998) Do
University, 4444 Forest Pa
3 (bases 1 to 116650)
Waterston, R.
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University, 4444 Forest
4 (bases 1 to 116650)
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Waterston, R.
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LOCUS AC004003 116650 bp
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21552. .21601,22478. .22639,29890. .29975,33855. .33944,
36395. .36488,39123. .39284,39881. .40218)
Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone CTA-437LI5 is from a release of the human BAC library CTB-HS-A. The library contains cloned DNA from human sperm. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8 (1996). The clone is available from VECTOR: pBeloBAC11
                                                                                                                                                                                                                                                           NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                    all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, sequence from more than one subclone; and regions were covered by confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the left is CTA-237G1. The actual start of this clone is at base position 1 of CTA-437L15; actual end is at 116650 of CTA-437L15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This chromosome 8 clone was provided by Dr. Patrick Concannon (patcon@vmmc.org) at the Virginia Mason Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted:
                                                                     Center: Washington University Genome Sequencing Center Center code: WUGSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone contains STS HS275YF1 (NID:g1051703).
Location/Qualifiers
                                                                                                                  Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------- Summary Statistics
                                                                                                                                                                                        Center project name: H_RG437L15
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'gene="WUGSC:H_RG437L15.1"
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150. 530
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/chromosome="8"
                                                 ---- Genome Center
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845. .4563
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/rpt_family="MaLR"
3188. .3348
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110. An'r
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KIADFCLSKWRMSLSQSRSSKSAPEGGTIIYMPPENYEPGGKSRASIKHDIYSYAVI
TWEVLSRKQPFEDVNNPLQIMYSVSQGHRPVINEESLPYDIPHRARMISLIESGWAQN
DDREPSEKCKLIELEPVLRTPEBITFLEAVIQLKKTKLQSVSSAIHLCOKKKMELSLN
IPVNHGPOEESCGSQLHENGSPETSRSLAPPQDDNETSRRAGOCYFWKLHCPGNH
SWDSTISGSQRAAFCDHKTTPCSSAIINPLSTAGOSRICGSRQSCHCOGGS
MTEACLNQSLDALLSRDLIMKEDYELVSTKPTRTSKVRQLLDTTDIGGEEFAKVIVQK
                                                                                                                                                             AVKHLHIHTPLLDSERKDVLREAEILHKARFSYILPILGICNEPEFLGIVTEYMPNGS
LNELLHRKTEYPDVAWPLRFRILHEIALGVNYLHNMTPPLLHHDLKTQNILLDNEFHV
                                                                                                                                           /translation="MNGEAICSALPTIPYHKLADLRYLSRGASGTVSSARHADWRVQV
/note="serine/threonine kinase RICK; match to protein AF027706 (NID:g3123886); H_RC437L15.1"
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                                                                                    /evidence=not_experimental
/protein_id="AAC24561.1"
/db_xref="G1:3264574"
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26268. .26500
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26611. .27000
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32329. .32460
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10435. .10540
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repeat_region	alignment_scores: Ouality: Ratio: Percent Similarity: alignment_block: US-09-445-223-1 x AC Align seg 1/1 to: A		428 39325 GACCTT 428 428 39425 CCCAGG 428

39574	428	39624	428	39674	428	39724	428	39774	428	39824	428	39874	443 39924	460 39974	477 40024	493 40074	510 40124	527 40174			13-JAN-1999 ce.	ata; Euteleostomi; .idae; Homo.	ute of Molecular , Germany .g. The start of thi
AAGTTATTTTGTTTATTTAACAAATTTGCAGGTATCTTTATATTTGAA		ATAAAATGGACATCAAACAAAACTGAACAAATCCCAGAAGATGGGAATGA		TGACATAAAGTGGTTTTTGCCCCGTGATTTATACCATAGGAAAAGGCAGT		GCCTTTTCTGGGGAGTGAGGGGGAGATAACCCAAATCTCTGAATGTTTCC		TGAAAATGACACCAT		CATAGGAAAATTATGTTTTATGCTTTATTTTTTTTTCATGGAATTTTACT		: TATTGCTATGTATCTGTCCTCACCTTTTAAATTATTCATTC	GluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSerLys :::	ArgGluaspileValasnGlnMetThrGlualaCysLeuAsnGlnSerLe 	uaspalaLeuLeuSerargaspLeuIleMetLysGluaspTyrGluLeuV	alserthrlysProThrArgThrSerLysValArgGlnLeuleuAspThr 	ThraspileGinGlyGluGluPheAlaLysValileValGlnLysLeuLy	SASPASNLYSGINMEtGlyLeuGInProTyrProGluIleLeuValValS 	9 erargserProserLeuAsnLeuLeuGlnAsnLysSerWet 540	e: gb_pr4:AF117829	men ON	ര ജര	
39525	4.28	39575	428	39625	428	39675	428	39725	428	39775	428	39825	429 39875	39925	460 39975	477	494	510	527 40175	sed_name	seq_docume LOCUS DEFINITION ACCESION VERSION KEYWORDS	SOURCE ORGANISM REFERENCE AUTHORS	TITLE JOURNAL COMMENT

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3282
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>mplemen+'^¬¬¬
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sequence (320001. .320250) overlaps with the start of the neighbouring Acc_number AF049895 (1. .250).
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                                  1. .320250

Organism. Homo sapiens"

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428		428
178994	CCCAGGAGATGGATGATGACATGGCCCCAAATGGTATTCTATGAACATC	179043
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179294	TGAAAATGACACCATTCCCCA	179343
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179394	TATTGCTATGTATCTGTCCTCACCTTTTAAATTATTCATTC	179443
4 4	GluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSerLys :::	443
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+ 6	AGGAAGACATTGTGAACCAAATGACAGAAGCCTGCCTTAACCAGTCGCT	7
460	uaspalaLeuLeuSerArgaspLeuIleMetLysGluAspTyrGluLeuV 	477 17.9593
477	alSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 	493 179643
464		510
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510	SASPASNLYSGINMEtGlyLeuGInProTyrProGluIleLeuValValValS 	527 179743
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sed_name	e: gb_rol:AF302127	
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VEKSION KEYWORDS	AF30212/.1 GI:1112043 house mouse	

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288 ACATICTACCIGIGIACCGCATAIGCCAGGAACCI.....GICGGCTIG 331
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LHLAACKELTEEKADVWARGPLNQTALHLAAARGHSEVVEELVSADLIDLSDEGGLSA
LHLAAQGRHSQTRLLKHGAHINLQSLRFQGGSSAATLLRRSKT"
901 c 1000 g 83.2 t
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FEREASTGDLGPTDIQKKKLVDAIISGDTSRLMKILQPQDVDLVLDSSASLLHLAVEA
GQEECVKWLLLNNANPNLTNRKGSTPLHMAVERKGRGIVELLLARKTSVNAKDEDQWT
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         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3559)
Chen, L., Haider, K., Cariappa, A., Rowitch, D. and Pillai, S. PKK, a novel ankyrin repeat-containing protein kinase regulated by protein kinase C-beta
                                                                                                                                          Unpublished
2 (bases 1 to 3559)
Chen, L., Haider, K., Cariappa, A. and Pillai, S.
Direct Submission
Submitted (01-SEP-2000) Cancer Center, Massachusetts General
Hospital, 149 13th Street, Charlestown, MA 02129-2060, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MetAsnGlyGluAla......IleCysSerAlaLeuProThrIl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47 Lys.....HisLeuHisIleHisThrProLeuLeuAspSerGluAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="PKC-regulated kinase PKK"
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Gaps: 27
Percent Identity: 33.816
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/organism="Mus musculus"
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/db_xref="taxon:10090"
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/codon_start=1
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.US-09-445-223-1 x AF302127
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GCCCGAGTCCTCAGCCTCAAGCGCGCCTCTGCTCCCCTTCGATAACG 1040
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271 erGlyTrpAlaGlnAsnProAspGluArgProSerPheLeuLysCysLeu 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288 IleGluLeuGluProValLeuArgThrPheGluGluIleThrPheLeuGl 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           304 uAlaValIleGlnLeuLysLysThrLysLeuGlnSerValSerSerAlaI 321
                                                                                                sThrGluTyrProAspValAlaTrpProLeuArgPheArgIleLeuH1sG : :: ||| ||||||||||:::||||
                         G......CCATTGCCTTGGGACCTGCGCTTTCGCATCGTGCACG
                                                                                                                                                                                                                            420 AGACAGCCGTGGGCATGAACTTCCTGCATTGCATGTCTCGCCACTGCTG
                                                                                                                                                                                                                                                                                                                            570 AGGACCTCAGCATG.....GATGGCCTGTTTGGTACAATCGCT
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                                                                                                                                                                                                  luIleAlaLeuGlyValAsnTyrLeuHisAsnMetThrProProLeuLeu
                                                                                                                                                                                                                                                                                                     HisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsnGluPheHisVa
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Bahr, C., Rohwer, A., Stempka, L., Rincke, G., Marks, F. and Gschwendt, M.
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                                                                                                                                                                                                                                                                                                                                  1163 AGGCTCTCGGGGGTGTCCTCAGTGGACTCAGCCTTTTCCTCCAGAG.... 1208
                                                                                                                                                                                                                                                                                                                                                                                                                       1323 TGAAGATCCTACAGCCCCAAGATGTGGACTTGGTTCTAGACAGCAGTGCC 1372
                                                               1062 TGT.....CACAGTTGG.....ACTCTGGGATCTCCCAGAC 1092
                                                                                                                                                        ........AAGGCCCCGAAGAGCTCAGCCGAAGTT... 1124
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                                                                                                                                                                                                                                                                                           437 n.....GlnTrpIleGlnSerLysArgGluAspIleV 448
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   465 SerArgAspLeulleMetLysGluAspTyrGluLeuValSerThrLysPr 481
                       387 sCysProGlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgA 404
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HOMO sapiens mRNA for protein kinase (dik gene).
AJ278016
                                                                                                                404 laAlaPheCysAspHisLysThrThrProCysSerSerAlaIleIleAsn
                                                                                                                                                                                                    421 ProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGlyIleAlaGl
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/9. 3843
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dlk gene; protein kinase.
human.
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Gschwendt, M.
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LISOLDSGYSGAVEGPRELSRSSSEXILPSSSSGKRLSGYSSYDSAFSSRGSILSFE
REPSTSDLGTTDVQKKKLVDAIVSGDTSKLMKILGPODVDLALDSGASLLHLAVEAGG
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HFAAONGDESSTRLLIEKNASVNEVDFEGRTPMHVACOHGORIVALLIERGYDVSLG
GKDAWIPLHYAANGGHLPIVKLLARQPGVSVNAQTLDGRTPLHLAAQRGHYRVARILI
DLCSDVNVCSLLAQTPLHVAARTGHTSTARLLLHRGAGKKAYTSDGYTALHLAARNGH
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18438. . 3843
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DFGLAKCNGLSHSHDLSMDGLFGTIAYLPPERIREKSRLFDTKHDVYSFAIVLWGVLT
                                                                                                                                                                                                                                                                                           OKKPFADEKNILHIMVKVVKGHRPELPPVCRARPRACSHLIRLMORCWOGDPRVRPTF
OEITSETEDLCEKPDDEVKETAHDLDVKSPPEPRSEVVPARLKRASAPTFDNDYSLSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 TGGCTTCGGAG......CCATTGCCATGGGATCTCCGGTTCCGA 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 IleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetThrPr 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         509 ACTACCACGTCAAGATTTCTGATTTTGGTCTGGCCAAGTGCAACGGGCTG 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 ArgPheSerTyrIlePheProlleLeuGlyIleCysAsnGluProGluPh 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 spSerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLysAla 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 GlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValG1 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                459 GCCACTCCTGCACCTCGAGCCCGCGGAACATCCTGCTGGATGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 nValAlaValLys......HisLeuHisIleHisThrProLeuLeuA
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411	5. AspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHisLysTh	395
394 1066	o inaspcysiyirnemetLysLeunishisCysProGiyasnHisSerirp ::	3/6
ä	0CCTCTGCCCCACCTTCG	101
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1009		986
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316	leT	300
883	1	871
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870		826
283		267
266 825	4 classpirerionyraspirerionisadapaargmecile ::	776
		1
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0	Two Corral a Drock Line 1 to	7

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Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1833)
Pazdernik, N. J., Donner, D. B., Goebl, M.G. and Harrington, M.A.
Mouse Interacting Protein 3 Does Not Contain a Caspase Recruiting or a Death Domain but Induces Apoptosis and Activates NF-kappaB Mol. Cell. Biol. 19 (1999) In press
2 (bases 1 to 1833)
Pazdernik, N. J., Donner, D. B., Goebl, M.G. and Harrington, M.A.
Direct Submission
Submitted (19-MG-1999) Walther Oncology Center, Indiana University School of Medicine, 1044 West Walnut Street, Indianapolis, IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="receptor interacting protein 3"
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                                                                                            475 uLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuA 492
                                                                                                                                                                                                                                                                                         509 LeuLysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuVa 525
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497 c 477 g 393 t
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AF178953.1 GI:6063100
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alignment_scores:

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Quality: 402.00 Length: 534 Ratio: 1.529 Gaps: 19 Percent Similarity: 49.251 Percent Identity: 27.154	alignment_block: US-09-445-223-1 x AF178953	Align seg 1/1 to: AF178953 from: 1 to: 1833	8 SeralaLeuProThrIleProTyrHisLysLeualaaspLeuArgTyrLe 24	24 uSerargGlyalaSerGlyThrValSerSerAlaArgHisAlaAspTrpA 41 ::::::	41 rgValGlnValAlaValLysHisLeuHisIleHisThrProLeuLeuAsp 57 ::::	58 SerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLysAlaAr 74	74 gPheSerTyrIlePheProlleLeuGlylleCysasnGluProGluPhe. 90	91LeuGlylleValThrGluTyrMetbroAsnGlySer 102	103 LeuAsnGluLeuLeuHisArgLysThrGluTyrProAspValAlaTrpPr 119 	119 oLeuargPheargIleLeuHisGluileAlaLeuGlyValasnTyrLeuH 136	136 isAsnMetThrProProLeuLeuHisHisAspLeuLysThrGlnAsnile 152	153 LeuLeuAspAsnGluPheHisValLysIleAlaAspPheGlyLeuSerLy 169 	169 sTrpargMetMetSerLeuSerGlnSerArgSerSerLysSerAlaP 185 ::::::	185 roGluGlyGlyThrIlelleTyrMetProProGlu	197 ASNTYrGluProGlyGlnLysSerArgAlaSerIleLysHisAspIleTy 213	213 rSerTyralaValIleThrTrpGluValLeuSerArgLysGlnProP 229	229 heGluaspValThrAsnProLeuGlnIleMetTyrSerValSerGlnGly 245 ::	246 HisargprovallleasnGluGluSerLeuProTyrasplleProHisar 262 :::

279 . 979 295 1011 307	323 1111 327 1161 340		4 5 9 9 B B B	468 1406 484 1448 . 1495	04-FEB-1998
262 galaArgMetIleSerLeuIleGluSerGlyTrpAlaGlnAsnProAspG ::::::::::::::::::::::::::::::::::::	eGlnLeuLysLysThrLysLeuGlnSerValSerSerAlaIleHisLeu. :::::	10 yproGlnGluGarCysGLySerSerGlnLeunisGlusanserGLyS 1111 :::::::::::::::::::::::::::::::::	990 GGTGGCACTCCTCACATACTTTACCCTTCACAGGCACAACAC 404AlaalapheCysaspHisLysThrThrProCysSerSeralaI 1349 CTGGGCCAGTCTTACTGAGACTCCCGGTCCTCACCC 418 lelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProGly 1386CCAAG 435 IleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGlnMe 1392 GAATCAGGGAGATGG	451 tThrGlualaCysLeuasnGlnSerLeuaspalaLeuLeuSerArgaspL 1406	495 p 495 1499 T 1499 seq_name: gb_pat2:168122 seq_documentation_block:
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1490		1539

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stanger, B. Z., Leder, P., Lee, T. H., Kim, E. and Seed, B. Rip: a novel protein containing a death domain that interacts with restARPO-1 (CD95) in yeast and causes cell death (4), 513-523 (1995) 95277818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 2268)
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Mus musculus cell death protein (RIP) mRNA, complete cds.
U25995
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                                                                                                                                                                                               1640 TIGGAAACCACAAITAIAIGGAIGIIGGACIGAAIICACAACCACCAAAC 1689
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                                                                                                       :::|||:::::||| :::
1590 AGCAGATGACCTCATAAAATATACTATATTCAATAGTTCTGGTATTCAGA 1639
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02115, USA
                                                                                                                                                          452 ThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLe
                                                                                                                                                                                                                                        468 ulleMetLysGluAspTyrGluLeuValSerThrLysProThrArgThrS
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                                                                                                                                                                                                                                                                                                                                                                                                       protein;
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52. .2022
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Fas; TNF receptor.
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443
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                                                                                                                                                                                                           8
                                                                                                                                                                                                       /note="apparent polymorphism resulting in a Thr variation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156 snGluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMet 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         594 CACCACTAAGAAGAAGAAGGTGGTACCCTTTACTACATGGCACCCGAAC 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 euLeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPhe 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ::||| |||||||:::
359 TGCTA.....AAGACCCAGATA...GATGTCCCACTTCATTGAAAGGA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              494 GTGACTITCACATIAAGATAGCCGATCTTGGTGTGGCTTCCTTTAAGACA 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 uPheLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 GAACTATICGCIGGIGAIGGAGIACAIGGAGAAGGGCAACCIGAIGCACG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 ArgileLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetTh 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              118 CTAGACAGCGGAGGCTTCGCGAAGGTGTCCTTGTTTACCACAGAAGCCA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 TGGATTTGTCATCCTGAAAAA......GTATACACAGGGCCCAACC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  259 CTGAGACACAGTCGAGTGGTGAAGCTACTGGGCATCATCATAGAAGAAGG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   400 AGGATAATCGTGGAGGCCATAGAAGGCATGTGCTACTTACATGAC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173 MetSer...LeuSerGlnSerArgSerSerLysSerAlaPro.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         139 rProProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24 LeuSerArgGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pArgValGlnValAlaValLysHisLeuHisIleHisThrProLeuLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57 spSerGluArgLysAspVal...LeuArgGluAlaGluIleLeuHisLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 AlaArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGl
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Gaps: 25
Percent Identity: 25.452
                                                                                                                                                                                                                                                                                                  /gene="RIP"
/note="silent polymorphism"
/replace="C"
490 c 577 g 482 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 2268
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                                                                                                                                                                                                                                                        /replace-"T"
                                                                                                                                                                                      /gene="RIP"
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51.232
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                                                                                                                                                                        variation
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ORIGIN
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e 208 . 681	r 225 : A 725	V 242 : 775	o 256 825	r 273 G 857	L 290 : T 907	a 305 T 954	e 316 G 1004	. 324 A 1054	y 340 	1 353 1154	. 360 G 1204	n 370 T 1254	i 387 A 1298	. 389 G 1348	a 405 T 1389	. 420 G 1439	G 432
7AsnTyrGluProGlyGlnLysSerArgAlaSerIl.	LysHisAspIleTyrSerTyrAlaValIleThrTrpGluValLeuSerAr ::: ::::::::: GACGTGTACAGCTTTGGCATTGGAAA	<pre>5 gLysGlnProPheGluAspValThrAsnProLeuGlnIleMetTyrSerV</pre>	alSerGlnGlyHisArgProVallleAsnGluGluSerLeuPro ::::::: :::	TyrAspileProHisArgAlaArgMetIleSerLeuIleGluSerGlyTr ::: AGGGAGATCATCAGCCTCATGGAGCGGTGCTG		euGluproValLeuArgThrPheGluGluleThrPheLeuGluAla 	<pre>valileGlnLeuLysLysThrLysLeuGlnSe ::: GTGGCAAGTTAAAGAAAGAGTATCCAGATCAAAGCCCAGTGCTGCAGAG</pre>	rValSerSerAlaIleHisLeuCys	5AspLysLysLysMetGluLeuSerLeuAsnIleProValAsnHisGly :::::::	_	3 uAsnSerGlySerProGluThr	SerArgSerLeuProAlaProGlnAspAsn		SCYSPTO	0GlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAla :::	<pre>PheCysaspHisLysThrThrProCysSerSerAlallelleAsn </pre>	1
19	209	225	242	257 826	273 858	290	306	316 1005	32.	341 1105	353 1155	361 1205	371 1255	387 1299	390 1349	406 1390	421

TCCAGTGCCAG
ACCAACATACCGGGAAGCACACCACCATGCCATACTTCTCTGGGCCAGT
444 .ArgGluAspIleval.AsnGlnMet
452 ThrGlualacysLeuAsnGlnSerLeuAspalaLeuLeuSerargaspLe 468 :: :: :: :::::::: 1640 TTGGAAACCACAATTATATGGATGTTGGAATTCACAACCACCAAAC 1689
468 uileMetLysGluAspTyrGluLeuValSerThrLysProThrArgThrS 485
485 erLysValargGlnLeuLeuAspThrThrAspIleGlnGlyGlu 499 :: ::: ::::: :::
500GluPhealaLysValileValG1 507 iiiii
507 nLysLeuLysAspasnLysGlnMet 515 :::::: ::::: 1840 ATCGATGAAATCGACCATGACTATG 1864
seq_name: gb_pat1:AR105328
seq_documentation_block: LOCUS AR105328 1557 bp DNA PAT 14-FEB-2001 DEFINITION Sequence 2 from patent US 6096539. ACCESSION AR105328 VERSION AR105328.1 GI:12818925 KEYWORDS GURNOWN.
Unclassified 1 (bases 1 Gomes, B.Char Protein acti Patent: US 6
SOUTCE 1153/ /Organism="unknown" BASE COUNT 395 a 422 c 448 g 291 t 1 others ORIGIN
alignment_scores: Quality: 395.00 Length: 499 Ratio: 1.452 Gaps: 21 Percent Similarity: 54.509 Percent Identity: 28.056
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Align seg 1/1 to: AR105328 from: 1 to: 1557
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27 yalaserGlyThrValSerSeralaArgHisAlaAspTrpArgValGlnV 44
44 alAlaValLySHisLeuHisIleHisThrProLeuLeuAspSerGluArg 60

us-09-445-223-1.p2n.rge

40		162
63	LysaspValLeuArgGluAlaGluIleLeuHisLysAlaArgPheSerTy 7 ::: :::: 	77 212
77	rllepheprolleLeuGlylleCysAsnGluProGluPhe	90
91	LeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGlu	105 312
.06	LeuLeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPh :	122 353
122	eArgileLeuHisGluileAlaLeuGlyValAsnTyrLeuHisAsnMetT	139
139	hrproproLeuLeuhisHisaspLeuLysThrGlnAsnileLeuLeuAsp :::	155 453
156	AsnGluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMe	172 501
172	tMetSerLeuSerGlnSerArgSerSerLysSerAlaProGluGlyGlyT:::::::::	189 544
189	hrileiletyrMetProProGluAsnTyrGluProGlyGlnLysSerArg ::: :: :: :: :: :: cccrGGGCTACTTGGCCCCAGAACTGTTTGTTAACGTAAACCGGAAG	205 591
206 592	AlaserileLysHisAspileTyrSerTyrAlaValileThrTrpGluVa 	222 641
222	lLeuSerArgLysGlnProPheGluAspValThrAsnProLeuGlnIleM ::: ::::: GCTTGCTGGAAGAGAAGTTGAGTTGCCAACCGAACCATCACTGT	239
239	ettyrSerValSerGlnGlyHisArgProVallleAsnGluGluSer:: :::	254 732
255	LeuProTyrAsplleProHisArgAlaArgMetlleSerLe	268 782
268 783	ullegluserglyTrpAlaglnAsnProAspGluArgProSerPheLeuL ::::: :::::::	285
285 833	yscysteulleGluLeuGluProvalLeuArgThrPheGluGluIleThr :: ::: :: ::: ::: ::: :::	301 876
302 877	PheLeuGlualaValIleGlnLeuLySLysThrLysLeuGlnSerValSe :::::: :::::::	318 926
318 927	rSer.AlaileHisLeuCysAspLysLysMetGlu	330
331	LeuSerLeuAsnIleProvalAs	338

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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Homo.

Eukaryota; Ho
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                                                                           1253 Greergeacecegaggaareaggggergagag......1286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1329 AGTAACAGGGCGACCGCTCGTTAACATATACAACTGCTCTGGGGTGCAAG 1378
                                                                                                                                                                                                                                                                         1153 GCAGGCACATCTTCAGATTCGATGGCCCAACCTCCCCAGACTCCAGAGAC 1202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1203 CTCAACTITCAGAAACCAGATGCCCAGCCCTACCTCAACTGGAACACCAA 1252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1287 ......ACAAGGCATGAACTGGTCCTGCAGGACCCGGAGCCAAATCC 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                                1103 TTACCAAGAGGAGCAGGGCACAAGAGGAGGAGGTTCCACAAGCCTGGACA 1152
977 AAATGGATGGCTTTAGGAGAACCATAGAAAACCAGCACTCTCGTAATGAT 1026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               378 .....GlnAsp 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              380 CysTyrPheMetLysLeuHisHisCysPro......GlyAsnHi 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 sSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspH 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 isLysThrThrProCysSerSerAlaIleIleAsnProLeuSerThrAla 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426 GlyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSe 442
                                                                                                                                                                                                                                  351 LeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPr 367
                                                                                                                                                                                                                                                                                                                                                                                        367 oGlnAspAsnAspPheLeuSerArgLysAla......
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Gaps: 21
Percent Identity: 28.056
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LOCUS AX067677 1557 bp DNA
DEFINITION Sequence 2 from Patent WO0077200.
ACCESSION AX067677
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US-09-445-223-1 x AX067677
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Ratio:
Percent Similarity:
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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40	CCTTGGTGCCATCGAGGAACTGGAGAACAGGAGGTGGTCGGCAAGGA	68
27	yalaSerGlyThrvalSerSerAlaArgHisAlaAspTrpArgValGlnV ::: CGGGTTCGGCACAGTGTTCCGGGCGCAACATAGGAAGTGGGGCTACGATG	44 139
44	alAlaValLysHisLeuHisIleHisThrProLeuLeuAspSerGluArg.	60 162
61 163	leLeuHisLysAlaAr ::: CCATGCCAAGTCTGGA	77 212
77	rilePheProlleLeuGlylleCysAsnGluProGluPhe	90
91	LeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGlu :::::: ::: CCAAGCCGGCTCTTGGTGAATTCATGGAGAACGGCTCCTTGTCGGG	105 312
313	LeuLeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPh :: :: CTGCTGCAGTCCCAGTGCCCTTGGCCCTGGCCGCTCCTTG	122 353
122 354	FT	139 403
139	hrProProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAsp::	155 453
156	AsnGluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMe	172 501
172 502	tMetSerLeuSerGlnSerArgSerSerLysSerAlaProGluGlyGlyT:::::::::::::::::::::::::::::::::	189 544
189 545	hrileiletyiMetProProGluAsnTyrGluProGlyGlnLysSerArg ::: :: ::: ::: ::: CCTGGGCTACTTGGCCCCAGAACTGTTGTTAACGTAAAACGGAAG	205 591
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255 733	LeuProTyrAspileProHisArgAlaArgMetileSerLe	268 782
268	ulledluserGlyTrpAlaGlnAsnProAspGluArgProSerPheLeuL :::::: ::::::	285 832
285	ysCysLeulleGluLeuGluProValLeuArgThrPheGluGluIleThr :: :: :: ::: ::: ::: :::	301 876
302	PheLeuGluAlaVallleGlnLeuLysLysThrLysLeuGlnSerValSe	318

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14-FEB-2001
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1329 AGTAACAGGGCGACCGCTCGTTAACATATACAACTGCTCTGGGGTGCAAG 1378
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                                                                                                                                                                                                                                                                                                                          367 oGlnAspAsnAspPheLeuSerArgLysAla......377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380 CysTyrPheMetLysLeuHisHisCysPro......GlyAsnHi 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   392 sSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspH 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     409 isLysThrThrProCysSerSerAlaIleIleAsnProLeuSerThrAla 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unknown.
Unknown.
Unknown.
Unclassified.
1 (bases 1 to 1873)
Gomes, B.Charles, Kasof, G.M. and Prosser, J.Caroline.
Frotein activator of apoptosis
Patent: US 6096539-A 1 01-AUG-2000;
Location/Qualifiers
318 rSer.AlaIle.....HisLeuCysAspLysLysMetGlu.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 rLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeu 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 501
Gaps: 22
Percent Identity: 28.144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAT
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Sequence 1 from patent US 6096539.
AR105327 GI:12818924
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1.443
54.291
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Quality:
Ratio:
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VERSION
KEYWORDS
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ORIGIN
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TITLE
. JOURNAL
FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
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alignment_block US-09-445-223-	_block: 5-223-1 x AR105327		•
Align seg	1 1/1 to: AR105327 from: 1 to: 1873		
11 204	ProThrileProTyrHisLysLeuAlaAspLeuArgTyrLeuSerArgGl 27 :: ::: :::::: :: :: cccrrggrgccarcgAggAacrGgAgAAcCAGGAGCTCGTCGCGAAAGG 253	ε.	
27	yalaserGlyThrValSerSeralaargHisalaaspTrpArgValGlnV 44 ::: ::: cGGGTTCGGCGACAACATAGGAAGTGGGGCTACGATG 303	n	
44	alalaValLysHisLeuHisIleHisThrProLeuLeuAspSerGluArg 60		
61	LysaspValLeuArgGluAlaGluIleLeuHisLysAlaArgPheSerTy 77	νο.	
77	rilePheProileLeuGlyIle	-	
87	10	т п	
104	AsnGluLeuLeuHisArgLysThrGluTyrPrOAspValAlaTrpProLe 12(::: ::: ::: rcGGGGCTGCTGCAGTGCCCTCGGCCCTGGCCGCT 51	4	
120	uargPheArgIleLeuHisGluIlealaLeuGlyValasnTyrLeuHisA 137 	4	
137	snMetThrProProLeuLeuHisHisAspLeuLysThrGlnAsn11eLeu 153 :::::::	4 3	
154	LeuaspasnGluPheHisValLysIlealaaspPheGlyLeuSerLysTr 170 [4	
170	pargmetMetSerLeuSerGlnSerArgSerSerLysSerAlaProGlug 187 :::	7 5	
187	1ydlyThrileIleTyrMetProProGluAsnTyrGluProGlyGlnLys 203	2 3	
204	SerargalaserileLysHisAspileTyrSerTyrAlaValileThrTr 220 :::	.2	
220	pgluvalleuserArgLysGlnProPheGluaspValThrAsnProLeuG 237	7 9	
237	<pre>lnllemetTyrSerValSerGlnGlyHisArgProVallleAsnGlu 252 ::: ::: ::: ::: ::: rcgrcraccaagcAgrcgaacAgcCagaAccgGcCrrcarrgGcrgAg 899</pre>	.2	
253	GluSerLeuProTyrAsplleProHisArgAlaArgMetil 266	66	
266	eSerLeuIleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerP 283 ::: :::::		

283 heLeuLyscysLeuIleGluI	heleuLyscysLeulleGluLeuGluProValLeuArgThrPheGluGlu 299	Valasn.HisGly	ysanisseritpasperintiescrityserentariance of the passerity passeri	Ax06/5676 1873 bp DNA PAT 19-JAN-2001 Ax06/5676 1873 bp DNA PAT 19-JAN-2001 Sequence 1 from Patent WO0077200. Ax06/7676 Ax06/7676 Ax06/7671 GI:12329570 human. Homo sapiens Butkaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml; Butkaryota: Metazoa; Chordata; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1873) Gomes, B.C., Kasof, G.M. and Prosser, J.C. Gomes, B.C., Kasof, G.M. and Prosser, J.C. Receptor interacting protein rips Patent: WO 0077200-A 1 21-DEC-2000; AstraZence AB (BS) Location/Qualifiers 1
			390 1414 407 1454 424 1490 440 1540 eq_name:	

204 CCCTTGGTGTCCATCGAGGAACTGGAGAACCAGGAGCTCGTCGGCAAAGG 253 |||| ::: |||||||:::: ::: /::: |
327 AAGGCGATATCCAGGGAGGTCAAGGCCATGGCAAGTCTGGATAACGAATT 376 ::::::: ::: 111:::
377 CGTGCTGCGCCTAGAAGGGTTTTATCGAGAAGGTCGGCTCGAGCTCAAG 426 87 luProGluPheLeuGlyIleValThrGluTyrMetProAsnGlySerLeu 103 104 AsnGluLeuLeuHisArgLysThrGluTyrProAspValAlaTrpProLe 120 170 pargMetMetSerLeuSerGlnSerArgSerSerLysSerAlaProGluG 187 665 TCAG.....GGAGGCTCACAGTCAGGGACAGGGTCCGGGAGCCA...G 705 187 lyGlyThrIleIleTyrMetProProGluAsnTyrGluProGlyGlnLys 203 SerArgAlaSerIleLysHisAspIleTyrSerTyrAlaValIleThrTr 220 pGluValLeuSerArgLysGlnProPheGluAspValThrAsnProLeuG 237 237 InIleMetTyrSerVal...SerGlnGlyHisArgProValIleAsnGlu 252 ::: ::: ::: ::: ::: |||| 27 27 yAlaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValGlnV 44 61 LysAspValLeuArgGluAlaGluIleLeuHisLysAlaArgPheSerTy 77 44 alAlaValLysHisLeuHisIleHisThrProLeuLeuAspSerGluArg 60CysAsnG 87 11 ProThrIleProTyrHisLysLeuAlaAspLeuArgTyrLeuSerArgGl Length: 501 Gaps: 22 Percent Identity: 28.144 353 to: 1873 /db_xref="taxon:9606" . 531 c 518 g from: 1 77 rIlePheProlleLeuGlyIle..... 392.50 1.443 54.291 Align seg 1/1 to: AX067676 alignment_block: US-09-445-223-1 x AX067676 471 a Quality:
Ratio:
Percent Similarity: alignment_scores: BASE COUNT ORIGIN 154 615 907 204 220 803

850	TCGTGTACGAAGCAGTGTGCAACAGGCAGAACCGGCCTTCATTGGCTGAG	899
253	GluSerL	266
006	CTGCCCCAAGCCGGGC	943
266	eSerLeulleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerP::: :::::: ::::	283
- α	he	0
994		1040
300	IleThrPheLeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSe	316
1041	:	1087
316	rValSerSer.AlaIleHisLeuCysAspLysLysLysMetGlu	330
1088		1137
331	LeuSerLeuAsnIlePro	336
1138		1187
337		348
1188		1237
349	SerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuPr	365
1238		1263
365	oAlaProGlnAspAsnAspPheLeuSerArgLysAla	377
1264	CGAGCCTTACCAAGAGGAGCAGGGCACAAGAGGAGCAGGTTCCACAAGCC	1313
377	:	377
1314	TGGACAGCAGGCACATCTTCAGATTCGATGGCCCCAACCTCCCCAGACTCC	1363
378		390
1364		1413
390		407
1414	CAC	1453
407	ysAspHisLy	423
1454	THE STATE STATES	1489
424	ThralaglyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIl	440
1490		1539
440	eGlnSerLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeu	456
1540	TGCAAGTTGGAGCAACAACTACTTGACTATGCAACAGACAACTGCCTT	1588

9e-18 9e-18 3e-18

468.19 464.87 464.87 464.35

312.00 312.00 312.00 312.00

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can interact with, intracellular mediators or modulators of inflammation, cell death and/or cell survival pathways, directly or indirectly. Cells can be modulated or mediated in inflammation, cell death or cell survival pathways or another intracellular signalling activity using B1. Conditions such as AIDS and cancer can be treated using B1. Antibodies, oligonucleotides and ribozymes can also be used to regulate the above
                                                                                                                                                                                                                                                                                                                                                               B1 protein; intracellular mediator; modulator; inflammation; cell death; cell survival pathway; intracellular signalling; AIDS; cancer; human; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Bl protein regulates cell death and cell survival pathways derivatives, DNA and antibodies, also regulate intracellular inflammation; for treating AIDS, cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention describes the isolation of a novel human B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetAsnGlyGluAlaIleCysSerAlaLeuProThrIleProTyrHisLy 17
                                                                                                                               seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA1999.DAT:X02558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLeuAlaAspLeuArgTyrLeuSerArgGlyAlaSerGlyThrValSerS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 649 A; 452 C; 449 G; 539 T; 9 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 540
Gaps: 0
Percent Identity: 100.000
  /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT:T85095 + /cgnl_8/gcgdata/geneseq/geneseqn/NA1999.DAT:X56279 + /cgnl_8/gcgdata/geneseqn/NA2000.DAT:X35105 + /cgnl_8/gcgdata/geneseq/geneseqn/NA1999.DAT:X39696 + /cgnl_8/gcgdata/geneseq/geneseqn/NA1991.DAT:X9324 + /cgnl_8/gcgdata/geneseq/geneseqn/NA1991.DAT:010324 +
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                                                                                                                                                                                             BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             971L-0121746.
971L-0121011.
971L-0121199.
                                                                                                                                                                                             X02558 standard; cDNA; 2098
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                                                                                                                                                                                                                                                                              (first entry)
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Ratio: 5.239
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US-09-445-223-1 x X02558
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P-PSDB; W92795.
                                                                                                                                                                       seq_documentation_block
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                                                                                                                                                                                                                                                                                                                        Human B1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9855507-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-1997;
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                                                                                                                                                                                                                                      -MODEL-frame+_p2n.model -DEV-xlp
-Q-/cgnl_1/USPTQ_spool/US09445223/runat_13062001_092033_29676/app_query.fasta_1.604
-Q-/cgnl_1/USPTQ_spool/US09445223/runat_13062001_092033_29676/app_query.fasta_1.604
-DEV_Geneseq_0401 -QFMT-fastap -SIPFIX=p2n.mg -GAPP=12.000
-QGAPEXT=4.000 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-GGAPPEXT=0.000 -GGAPEXT=0.050 -XGAPD=10.000 -XGAPEXT=0.500
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-FGAPP=6.000 -DELEXT=7.000 -START=1 -MATRIX=bloopexpct
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_CORRE-pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFNT=pfs
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                                                                               About: Results were produced by the GenCore software, Copyright (c) 1993-2000 Compugen Ltd.
OM of: US-09-445-223-1 to: N_Geneseq_0401:*
                                                                                                                                                                                                                                                                                                                                                           NORM-ext -MINLEN-0 -MAXLEN-200000000
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Database sequences: 678276
Database length: 291890651
                                                                                                                                                                                                                                                                                                                                                                                                                                            Search information block:
Query: US-09-445-223-1
Query length: 540
                                         Date: Jun 13, 2001 6:38
                                                                                                                                            Command line parameters:
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Database 1
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protein which

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                  laProGluGlyGlyThrIleIleTyrMetProProGluAsnTyrGluPro
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ACTOGCOGACCTGCGCTACCTGAGCCGCGCGCGCCTCTGGCACTGTGTCGT
                                                        IleHisThrProLeuLeuAspSerGluArgLysAspValLeuArgGluAl
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phosphorylation effector; PHSP; proliferative disorder; disorder; neuronal disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA2000.DAT:246143
                                    hrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluGlu
                                                                        oGlnAspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMetL
                                                                                  ysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGly
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                                                                                                                                                                                                                                                                                          pLeuIleMetLysGluAspTyrGluLeuValSerThrLysProThrArgT
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203..1825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block
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human phosphorylation effectors useful for the diagnosis, treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                  246138-246168 encode human phosphorylation effectors (PHSP), designated PHSP1-PHSP31 (the protein sequence for PHSP28 is not given in the specification). The sequences were isolated from cDNA libraries prepared from various human tissues. The PHSP proteins are useful for the diagnosis, treatment and prevention of proliferative disorders, immune disorders and neuronal disorders. The PHSP proteins form pharmaceutical compositions which useful for treating or preventing disorders associated with decreased PHSP expression/activity. PHSP antagonists are useful for treating or preventing disorders associated with increased PHSP expression/activity.
                                                                                                                                                                                                                                                            Baughn MR;
H, Azimzai Y;
                                                                                                                                                                                                                                                                                                                                                                              and prevention of proliferative, immune and neuronal disorders
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                                                                                                                                                                                                                                                         Lal P, Tang YT, Corley NC, Guegler KJ, Bandman O, Au-Young J, Gorgone GA, Yue
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                                                                                                            98US-0152814.
98US-0173482.
98US-0106889.
                                                                                                                                                      98US-0109093.
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                                                                                                                                                                                                                                                        Hillman JL, Lal P, Tang Y.
Patterson C, Bandman O, A
Reddy R, Lu DAM, Shih LL;
                                                                    99WO-US17132
                                                                                               98US-0123494
                                                                                                                                                                                                                              (INCY-) INCYTE PHARM INC.
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Percent Similarity: 100.000
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            WO200006728-A2
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                                                                    28-JUL-1999
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14-OCT-1998
                                                                                                                                         03-NOV-1998
19-NOV-1998
                                                                                               28-JUL-1998
                                                                                                                                                                       22-DEC-1998
                                                                                                                                                                                     12-JAN-1999
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                                         10-FEB-2000
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1153 TTCAAGTGCCATTCACCTATGTGACAAGAAAATGGAATTATCTCTGA 1202
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                                                                                                                                                                                                                                                                                                                                 uSerLysTrpArgMetMetSerLeuSerGlnSerArgSerSerLysSerA 184
84 leCysAsnGluProGluPheLeuGlyIleValThrGluTyrMetProAsn 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           603 ACCIGCACAATATGACTCCTTTAACTTCATCATGACTTGAAGACTCAG
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                                                                                                                                                                                                                                                                                                                                                                                                      184 laProGluGlyGlyThrIleIleTyrMetProProGluAsnTyrGluPro
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                                                                                                                               aTrpProLeuArgPheArgIleLeuHisGluIleAlaLeuGlyValAsnT
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               453 TTTGCAATGAGCCTGAATTTTTGGGAATAGTTACTGAATACATGCCAAAT
                                                                             GlySerLeuAsnGluLeuLeuHisArgLysThrGluTyrProAspValAl
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Rosen CA, Ruben SM;
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                                                        P-PSDB; B43570
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dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; cancer associated gene; cancer antigen; detection; cancer;
                                                        1603 CTTGATCATGAAAGAGGACTATGAACTTGTTAGTACCAAGCCTACAAGGA 1652
                                                                                                                     434
                                                                                                                                                                               lyllealaglnGlnTrpIleGlnSerLysArgGluAspIleValAsnGln 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA2000.DAT:C77779
                                                                                                                                                                                                                                                                                                                                                                                                                                                uGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsnL
384 ysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGly
                                                                                                                       417 allelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cancer associated gene sequence SEQ ID NO:173
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E43398 to B44239. The proteins can have activities based on the tissues and cells the genes are expressed in. Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antialterative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antialterative; untibacterial; antiviral; dermatological; antialteratic; antibacterial; antiviral; dermatological; cantipatorial; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antiangiogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions. Polynucleotides, polypeptides, antibodies, agonists and antagonists from the present condition may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune calls, to treat disorders of haemacopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and sateagonists may be also be used in drug screens. C78449 to C78457 and the present sequences used in the exemplification of the present
Novel isolated nucleic acids comprising sequences encoding peptides useful for treating or diagnosing e.g. cancer \,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2709 BP; 810 A; 580 C; 540 G; 769 T; 10 other;
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Percent Identity: 99.815
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                                                                                                        Claim 1; Page 751-752; 2352pp; English.
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Percent Similarity: 100.000
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1067 TCTAATAGAAAGTGGATGGGCACAAAATCCAGATGAAAGACCATCTTTCT
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                                                                                                                                                                                                  ThrPheLeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSerVa
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                                                                                                                           laProGluGlyGlyThrIleIleTyrMetProProGluAsnTyrGluPro
                                                                                                                                                          GlyGlnLysSerArgAlaSerIleLysHisAspIleTyrSerTyrAlaVa
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CARD-3; caspase recruitment domain; CARD-4; regulation; detection. caspase activation; detection; screening; therapy; diagnosis; disease; apoptotic cell death; Fas/APO-1 receptor complex; TNF receptor complex; cancer; follicular lymphoma; carcinoma; p53 mutation; viral infection; hormone-dependent tumour; autoimmune disorder; Alzheimer's disease; systemic lupus erythematosis; immune-mediated glomerulonephritis; stroke; Parkinson's disease; amyotrophic lateral sclerosis; retinitis pigmentosa; spinal muscular dystrophy; cerebellar degeneration; anaemia; drug; myelodysplastic syndrome; myocardial infarction; cell proliferation; cell differentiation; cell survival; CARD-41; CARD-45; CARD-47;
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                                                                                                                                                                                                                                                      hrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluGlu
allelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProG
                                                434 lyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGln
                                                                                                   MetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAs
                                                                                                                                                     pLeuIleMetLysGluAspTyrGluLeuValSerThrLysProThrArgT
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214..1836
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98US-0019942.
98US-0099041.
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ID Z09246 standard; cDNA; 1931
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06-FEB-1998;
17-JUN-1998;
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crutisment domain, CARD-3 and CARD-4 polynucleotides and proteins of recruitment domain, CARD-3 and CARD-4 polynucleotides and proteins of partial murine CARD-4 protein and genes. The genes and proteins of the invention are involved in the regulation of caspase activation.

CC the invention are involved in the regulation of caspase activation.

The caspase recruitment domain (CARD) polynucleotides, polypeptides, complex predictive medicine and therapeutic and prophylactic methods of assays, predictive medicine and therapeutic and prophylactic methods of creatment. The methods may be used to diagnose and treat patients which are suffering from a disorder associated with abnormal level or rate of are suffering from a disorder associated with abnormal level or rate of complex, abnormal activity of the Fas/APO-1 receptor.

CC complex, abnormal activity of the Fas/APO-1 receptor complex, abnormal activity of the raspector complex, or abnormal activity of a caspase. Diseases that may be treated include cancer cartivity of a caspase. Diseases that may be treated include cancer (particularly follicular lymphoma, carcinomas associated with mutations in p53 and hormone-dependent tumours), autoimmune disorders (e.g. carticularly follicular lymphoma, carcinomas associated with mutations systemic lupus erythematosis, immune-mediated glomerulonephritis), viral infections, Alzeheimer's disease, Parkinson's disease, amyotrophic lateral collections, Alzeheimer's disease, Parkinson's disease, amyotrophic lateral collections, Alzeheimer's disease, parkinson's disease, anyotrophic lateral collections, ansemia, myclodysplastic syndrome, myocardial infarction, and strucke. CARD-3 protein interacts with other cellular proteins, and so can be used for regulation of cellular proliferation and differentiation and cell survival. The CARD-4 proteins may also be used to for screen drugs or compounds which modulate their activity. The CARD-4 gene can express a compounds which modulate their activity and CARD-4. This sequence conduction tha 
                                                                                                                                                                                 Novel CARD-3 and CARD-4 genes and polypeptides used or treating regulation of cellular proliferation and differentiation and cell
                                                                                                                                                                                                                                                                                                                 Example 2; Fig 1; 181pp; English
                                                                                       WPI; 1999-494269/41
                                                                                                                        P-PSDB; Y31140
                          Bertin J;
                                                                                                                                                                                                                                                           survival
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describes the isolation of novel human caspase

Sequence 1931 BP; 613 A; 429 C; 416 G; 473 T; 0 other;

Length: 540 Gaps: 0 Percent Identity: 99.630 Quality: 2817.00 Ratio: 5.226 Harity: 99.815 alignment_block: US-09-445-223-1 x Z09246 Percent Similarity: alignment_scores

to: 1931 from: 1 Align seg 1/1 to: 209246

- 114 ATGAACGGGGAGGCCATCTGCAGCGCCCTGCCCACCATCCCTACCACAA 263 1 MetAsnGlyGluAlaIleCysSerAlaLeuProThrIleProTyrHisLy
- 34
- 314 CCGCCCCCCCACGCAGGCTGGCGCGTCCAGGTGGCCGTGAAGCACCTGCAC 363 eralaargHisAlaaspTrpargValGlnValAlaValLySHisLeuHis 34
- 364 ATCCACACTCCGCTGCTCGACAGTGAAAGAAAGGATGTCTTAAGAGAAGC 413 67 IleHisThrProLeuLeuAspSerGluArgLysAspValLeuArgGluAl 21
- aGluIleLeuHisLysAlaArgPheSerTyrIlePheProIleLeuGlyI 84
- leCysAsnGluProGluPheLeuGlyIleValThrGluTyrMetProAsn 100 84

334 snileProValAsnHisGlyProGlnGluGluSerCysGlySerSerGln 350 ysLeuHisHisCysProGlyAsnHisSerTrpAspSerThr11eSerGly 400 284 euLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGluIle 300 367 oGlnAspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMetL 384 563 613 663 167 AATATCTTATTGGACAATGAATTTCATGTTAAGATTGCAGATTTTGGTTT 713 uSerLysTrpArgMetMetSerLeuSerGlnSerArgSerSerLysSerA 184 laProGluGlyGlyThrIleIleTyrMetProProGluAsnTyrGluPro 200 813 217 AsnGluGluSerLeuProTyrAspIleProHisArgAlaArgMetIleSe 267 267 rLeuIleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerPheL 284 117 134 317 ISerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeuA 301 ThrPheLeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSerVa LeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPr 514 GGATCATTAAATGAACTCCTACATAGGAAAACTGAATATCCTGATGTTGC aTrpProLeuArgPheArgIleLeuHisGluIleAlaLeuGlyValAsnT yrLeuHisAsnMetThrProProLeuLeuHisHisAspLeuLysThrGln AsnileLeuLeuAspAsnGluPheHisValLysIleAlaAspPheGlyLe GlyGlnLysSerArgAlaSerIleLysHisAspIleTyrSerTyrAlaVa GlySerLeuAsnGluLeuLeuHisArgLysThrGluTyrProAspValAl 351 384 134 117 564 614 151 664 167 714 184 764 201

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useful for treating diseases
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    RICK; human; RIP-like interacting CLARP kinase; apoptosis regulator; ARC; caspase-8; caspase-10; CD95 signalling; apoptosis signalling pathway; CIDE-8; CIDE-8; CIDE-8; cell growth; apoptosis dysregulation; gene therapy; cardiac disorder; cancer; neurodegenerative disorder; AIDS; aplastic anaemia; ischaemic injury; toxin-induced liver disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Compositions for identifying apoptosis signalling pathway inhibitors
                                                                                                                                                                        1364 AGCTGCATCACTGTCCTGGAAATCACAGTTGGGATAGCACCATTTCTGGA 1413
                                                                                                                      1464 AATAATAAATCCACTCTCAACTGCAGAAACTCAGAACGTCTGCAGCCTG 1513
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                             SerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSerAl
                                                                                          allelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProG
                                                                                                                                                                                                                                                                                   pLeuIleMetLysGluAspTyrGluLeuValSerThrLysProThrArgT
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                                                            1414 TCTCAAAGGGCTGCATTCTGTGATCACAAGACCATTCCATGCTCTTCAGC
                                                                                                                                                      434 lyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGln
                                                                                                                                                                                                                     MetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248762 standard; cDNA; 2502 BP
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This sequence encodes the human RICK (RIP-like interacting CLARP kinase)

Cof apoptosis, potentiating apoptosis induced by caspase-8 and caspase-10

during CD95 signalling. The invention provides methods for identifying

apoptosis signalling pathway inhibitors and activators, and methods and

compositions for screening compounds which will modulate the interactions

cof the various compositions identified: ARC, RICK, and the CIDE family of

activators (CIDE-A, CIDE-B and DREP-1). RICK is useful in screening

compositions for agents, useful in the diagnosis, prognosis or treatment of

disease associated with excess cell growth and dysregulation of

apoptosis. Complexes containing RICK and CLARP can be used in drug

screening assays to identify inhibitor molecules blocking CD95-mediated

cof apoptosis. Overspression of ARC in an in vitro cell system can be used

cof identify inhibitors of the enzymatic activity of caspase-8.

Cof identify inhibitors of the enzymatic activity of caspase-8.

Cof identify inhibitors of the enzymatic activity of caspase-8.

Cof identify inhibitors of the preparation of Identian in witer of capped and cardiac disorders. Therapeutic compositions of CIDEs can be used to

creat e.g. cancer, AIDS, neurodegenerative disorders, aplastic anaemia,

can dead as reagents for the preparation or affinity chromatography

media, and for diagnostically measuring RICK levels. A specific inhibitor

cof an essential step in the biochemistry of apoptosis is needed. RICK

interaction with intracellular factors such as CLARP and FADD appears

cof an essential for apoptosis, inhibitors of KICK binding to intracellular

cof peppeosis factors are potential drug candidates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 IleCysAsnGluProGluPheLeuGlyIleValThrGluTyrMetProAs 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2502 BP; 769 A; 535 C; 499 G; 699 T; 0 other;
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Percent Identity: 99.445
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Claim 8; Fig 7b; 93pp; English.
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Ratio: 5.200
Percent Similarity: 99.815
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US-09-445-223-1 x 248762
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                                                                                    150 nAsnIleLeuLeuAspAsnGluPheHisValLysIleAlaAspPheGlyL 167
                                                                                                                                                                                                                                                                                                                                                                                                   eAsnGluGluSerLeuProTyrAspIleProHisArgAlaArgMetIleS
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                                                                                                    675 GAATATCTTATTGGACAATGAATTTCATGTTAAGATTGCAGATTTGGTT
                                                                                                                                             euSerLysTrpArgMetMetSerLeuSerGlnSerArgSerSerLysSer
                                                                                                                                                                                                      184 AlaProGluGlyGlyThrIleIleTyrMetProProGluAsnTyrGluPr
                                                                                                                                                                                                                      AsnileProValAsnHisGlyProGlnGluGluSerCysGlySerSerGl
575 CTTGGCCATTGAGATTTCGCATCCTGCATGAAATTGCCCTTGGTGTAAAT
                             134 TyrLeuHisAsnMetThrProProLeuLeuHisHisAspLeuLysThrGl
                                           625 TACCTGCACAATATGACTCCTCTTTACTTCATCATGACTTGAAGACTCA
                                                                                                                                                                           725 TATCAAAGTGGCGCATGATGTCCCTCTCACAGTCACGAAGTAGCAAATCT
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New human breast and ovarian cancer associated gene sequences and the polypeptides encoded by these genes, useful in the prevention, treatment and diagnosis of cancer, immune disorders, cardiovascular disorders and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive; nootropic; neurpprotective; antiviral, antiallargic; hepatotropic; antidiabetic; antidiflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human breast and ovarian cancer associated antigen gene SEQ ID 228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Addison's disease; allergy; autoimmune haemolytic anaemia; autoimmune thyroiditis; diabetes mellitus; Crohn's disease; multiple sclerosis; rheumatoid arthritis; ulcerative colitis; cardiovascular disorder; wound healing; neurological disease;
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                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA2000.DAT:F21841
             spLeulleMetLysGluAspTyrGluLeuValSerThrLysProThrArg
                                                                                                                                         ACTIGATCATGAAAGAGGACTATGAACTIGTTAGTACCAAGCCTACAAGG
                                                                                                                                                                                  uPheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGlyL
                                                                                                                                                                                                                                        euGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsn
                                                                                                                                                                 ThrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluGl
                                                      nMetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgA
GlyIleAlaGlnGlnTrpIleGlnSerLysArgGluAspIleValAsnGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                           F21841 standard; DNA; 463
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434
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261161;

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Dreast and ovarian cancer associated DNA, protein, agonist or antagonist sequences exhibit cytostatic; immunosuppressive; nootropic; neutroprotective; antiviral; antiviral; hepatotropic; antidiabetic; antifinfammatory; antiviral; vulnerary; anticonvulsant; antibacterial; antifinfammatory; antidoer; vulnerary; anticonvulsant; antibacterial; antifingal; artiparasitic and cardiant activity. The polynucleotide and protein sequences are used in the diagnosis of cancer, particularly breast and ovarian cancer. The nucleic acid sequences, proteins, agonists and agonists may also be used in the diagnosis, prevention and treatment of immune disorders e.g. Addison's disease, allergies, autoimmune hamolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's cardiovascular disorders such as myocardial ischemmias; wound healing; neurological diseases such as cerebral anoxia and epilepsy; and
Sequences F21614 - F22031 represent DNA sequences encoding human proteins
                          B58711 - B59128. The DNA and protein sequences are associated with breast and ovarian cancer. Included in the invention are sequences F22032 - F22040 and B59129 which are used in the isolation and characterisation of the DNA and protein sequences of the invention. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infectious diseases.
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Sequence 463 BP; 150 A; 92 C; 89 G; 131 T; 1 other;

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Percent Identity: 99.333
               Length:
                                                                                                         Align seg 1/1 to: F21841 from: 1 to: 463
                        5.349
              797.00
                                                              alignment_block:
US-09-445-223-1 x F21841
               Quality:
                                     Percent Similarity:
                            Ratio:
alignment_scores:
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52 3 TACATGCCAAATGGATCATTAAATGAACTCCTACATAGGAAAACTGAATA 97 TyrMetProAsnGlySerLeuAsnGluLeuLeuHisArgLysThrGluTy

113 rProAspValAlaTrpProLeuArgPheArgIleLeuHisGluIleAlaL 130

147 LeuLysThrGlnAsnIleLeuLeuAspAsnGluPheHisValLysIleAl 163 rSerTyrAlaVallleThrTrpGluValLeuSerArgLysGlnProPheG 230

Gaps: 26 Percent Identity: 34.074

54.444 579.00 1.969

Percent Similarity:

Quality:

alignment_scores:

Ratio:

to: 2370

from: 1

to: 261161

Align seg 1/1

alignment_block: US-09-445-223-1 x 261161

Length:

seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA2000.DAT:261161

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Z61161 standard; DNA; 2370 BP.
seq_documentation_block:
                   ΩĪ
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The present sequence encodes a murine death associated kinase protein, containing ankyrin repeats, designated DAKAR. The DAKAR polynuclectides can be used to express the polypeptides, and as probes to identify nucleic acids encoding proteins having kinase activity. DAKAR polypeptides and fragmented polypeptides are used for purifying proteins, e.g. to measure protein activity; as quality assurance agents to monitor shelf life and stability of binding partner proteins; as research agents, e.g. in assays to determine protein kinase activity, to identify novel molecules involved in signal transduction pathways, and to identify therapeutic compounds which may interfere with apoptosis; as molecular weight and isoelectric focusing markers; as controls for peptide fragmentation; identification of unknown proteins, e.g. by comparison with proteins in databases; and for preparation of antibodies. The antibodies can be used in assays to detect the presence of the protein, and to purify the protein by immunoaffinity chromatography. The antibodies can also be used to block binding of the DAMAR polypeptides to their binding partners. Compounds that inhibit the protein a business activity of DAMAR can be used to treat diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel death associated kinase containing ankyrin repeats (DAKAR) used as molecular weight marker and as controls for peptide fragmentation
                                                                                                                       Death associated kinase protein containing ankyrin repeats; DAKAR; kinase; quality assurance agent; shelf life; marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             production or DAKAR.
                                                                                      DNA encoding a death associated kinase with ankyrin repeats.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             characterized by overproduction or upregulated
                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 9-10; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0095269.
98US-0099973.
99US-0119353.
                                                                                                                                                                                                                                                                                                                                                                                    99WO-US17576
                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-195582/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Virca GD;
                                                                                                                                                                                                                                                                                                             WO200008177-A2.
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                                                                                                                                                                                                                                                                                                                                                                                    04 - AUG-1999;
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11-SEP-1998;
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                                                  30-MAY-2000
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10	LeuProThrIleProTyrHisLysLeuAlaAspLeuArgTyrLeuSerAr 	26 98
26 99	gGlyAlaSerGlyThrValSerSerAlaargHisAlaAspTrpArgValG ::: ::::: ::: GGGGGGCTTCGGGCAGGTGTACAAGGTGCGCCATGTGCACTGGAAGGACGT	43 148
43	<pre>lnValAlaValLysHisLeuHisIleHisThrProLeuLeu ::: :: GGCTGGCGATCAAGTGCTCGCCCAGTCTGCACGTCGAC</pre>	56 186
57 187	AspserGluargiysAspvalLeuargGlualaGlulleLeuHisLysAl 	73 236
73	aArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGluP ::: ::: ::	90
90	heLeuGlylleValThrGluTyrMetProAsnGlySerLeuAsnGluLeu :::	106 330
107 331	LeuHisargLysThrGluTyrProAspValAlaTrpProLeuArgPheAr :::	123 368
123 369	ale 	140 418
140 419	roproteuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsn 	156 468
157 469	GluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMetMe :::::: :::	173 518
173 519	tSerLeuSerGlnSerArgSerSerLysSerAlaProGluGlyG 	188 556 ·
188 557	lythrileilefyrmetbroProGludanfyrGlubroGlyGlnLysSer 	204
205 601	ArgalaSerileLysHisAspileTyrSerTyralaValileThrTr 	220 650
220 651	pGluValLeuSerArgLysGlnPrOPheGluAspValThrAsnProLeuG 	237
237 701	IntleMetTyrSerValSerGlnGlyHisArgProValIleAsnGluGlu::	253 738
254 739	SerLeuProTyrAspIleProHisArgalaArgMetIleSe	267 788
267 789	rLeulleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerPheL:!!!:::::	284 831
284 832	euLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGluIle	300 846
301	ThrPheLeuGluAlaValIleGlnLeuL	317

	847 2	111 ACC	49
	17	ISerSerAlalleHisLeuCysAspLysLysLysMetGluLeuSerLeuA	m
	850	tctgaaacagaagactttgtgagaagcctgatgaggaggtgaaa 8	94
	334 8	snIleProValasnHisGlyProGlnGluGluSerCysGlySerSerGln 3 :::	350 939
	351 I	LeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPr 3 :: ::	367 989
	367 0	oGInAspAsnAsp.PheLeuSerArgLysAlaGlnAspCysTyrPheMet 3	383 1021
	384 1	LysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGl 4	400 1041
	400 3	cThrProCysSerSerA :::	417 1076
	417]		433 1111
	434 0		444 1161
	1162	gGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuA 4 :: TCCAGAGGATCGCTGTC	461 1178
	461 8	sphlaLeuLeuSerArgAspLeulleMetLysGluAspTyrGluLeuVal 4 ::: ACTGTCTTTTGAGC	477 1192
	478 :		4 93 1221
	494		510 1271
	510 :	saspasnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValValS : :::::: cagcaggcTGaTGaAGACCCCAAGATGTGGACTTGGTTCTAG]	527 1321
	527	erArgSerProSerLeu 532 :: ACAGCAGTGCCAGCCTG 1338	
sed	_name:	/cgn1_8/gcgdata/geneseq/geneseqn/NA2000.DAT:261784	
seq.	i	documentation_block: 261784 standard; cDNA; 3516 BP.	
X Y X	261784;	4;	
T X	27 - M.	27-MAR-2000 (first entry) Anna encoding murine protein kinase/ankurin homologue. S	SEO 1D NO:257
K K K X X	Skin	keratinocyte; neonatal foreskin keratinocyte stem cell; transit a ine; inflammation; cancer; neurolo	fibroblast; mplifying cell gical disease;

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73 aArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGluP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate angiogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences 261606-261812 represent cDNA sequences derived from 261725-261765, 261801 and 261826 encode proteins with an N-terminal signal sequence, indicating that the proteins are secreted. Sequences 261650-261688, 261766-261817 and 261812-261817 and 261827-261829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to novel nucleic acid sequences derived from rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murison JG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotides useful for the treatment of various conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encode proteins with one or more putative transmembrane domains
angiogenesis; tumour vascularisation; growth disorder;
developmental disorder; skin wound; hair follicle disorder;
anti-inflammatory; cytostatic; neuroprotective; vulnery; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93 GGGCGCCTTCGGGCAGGTGTACAAGGTGCGCCATGTGCACTGGAAGACGT 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kumble A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26 gGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 lnValAlaValLys......HisLeuHisIleHisThrProLeuLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3516 BP; 810 A; 886 C; 988 G; 832 T; 0 other;
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Gaps: 26
Percent Identity: 34.074
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 158-159; 235pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Watson JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: Z61784 from: 1
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention
                                                                                                                                                                                                                                                                                                                                               29-APR-1998;
09-NOV-1998;
                                                                                                                                                                    W09955865-A1
                                                                                                                                                                                                                                                                                     29-APR-1999;
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143 GGCTCGCGATCAAGTGCTCGCCCAGTCTGCACGTCGAC.

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.....ACCTTCCAAGAATT 840
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                                                                                                                                                                                                                                                                                                                                glleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetThrP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    513 GICCCACTCTCATGACCTCAGCATG......GATGGCCTGTTTG 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     205 ArgAla...SerIleLysHisAspIleTyrSerTyrAlaValIleThrTr 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              645 GGGTGTGCTTACACAGAAGCCATTTGCAGATGAAAGAACATCCTAC 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            733 CTGCCACCCATCTGCAGACCCCGGCCGCGTGCCTGTGCCAGCCTGATAGG 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               284 euLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGluIle 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       snIleProvalAsnHisGlyProGlnGluGluSerCysGlySerSerGln 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       367 oGlnAspAsnAsp.PheLeuSerArgLysAlaGlnAspCysTyrPheMet 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMetMe 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tSerLeuSerGlnSerArgSerSerLysSerAlaProGluGly.....G 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 lyThrIleIleTyrMetProProGluAsnTyrGluProGlyGlnLysSer 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pGluValLeuSerArgLysGlnProPheGluAspValThrAsnProLeuG 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 InIleMetTyrSerValSerGlnGlyHisArgProValIleAsnGluGlu 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 SerLeuProTyrAspIleProHisArg......AlaArgMetIleSe 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rLeuIleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerPheL 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301 ThrPheLeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSerVa 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                317 lSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerLeuA 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             351 LeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPr 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        783 GCTCATGCAACGGTGCTGGCATGCAGACCCACAGGTGCGGCCC.....
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90 heLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluLeu
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57
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Murison JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV; noctropic; neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1266 CACCAGGCTGATGAAGATCCTACAAGATGTGGACTTGGTTCTAG 1315
                                                                                                                1216 ACAGACATCCAGAAGAAGAAGCTAGTGGATGCCATCATATCAGGGGACAC 1265
                                                                                                                                                                                                                                                                                                                                                                                                                   Kumble KD,
                                                                                                                                                                                   ..........AATGCAAGCTCCCATCGTCCA 1105
                                                                                                                                                                                                                                                                                                                               461 spAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeuVal 477
                                         384 LysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGl 400
                                                                                                                                                                                                                                                                                                                                                                                         478 SerThrLysProThrArgThrSerLysValArgGlnLeu..LeuAspThr 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        510 sAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValValS 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA2001.DAT:C99717
                                                                                                                                                                                                                                                                                                     1156 TCCAGAG......GATCGCTGT......C
                                                                                                  400 ySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSerA
                                                                                                                                                        417 lallelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro
                                                                                                                                                                                                                  GlylleAlaGln...........GlnTrpIleGlnSerLysAr
                                                                                                                                                                                                                                            1106 GCAGTGGCAAGAGGCTCTCGGGGGTGTCCTCAGTGGACTCAGCCTTTTCC
                                                                                                                                                                                                                                                                       gGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuA
                                                                       .....CACAGITGG.....ACICIGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                  494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLy
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            .....ccgagrigc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammation; neurological disease; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skin cell cDNA, SEQ ID NO: 257.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
ID C99717 standard; cDNA; 3516
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 984 CTTCGATAACGACTGCAGTCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1316 ACAGCAGTGCCAGCCTG 1332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  527 erArgSerProSerLeu 532
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                                                                                                                               1036 ATCTCCCAGACTCTTG..
                                                                                                                                                                                     CCGAAGTT...CCTCTG
                                                                                                                                                                                                                                                                                                                                                               1173 ACTGTCTTTTGAGC
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                                                                       1016
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The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth.of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV)-1 to leukocytes, and treating inflammantory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of oligonucleotides for examining expression patterns.
                                                                        New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 gileLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetThrP 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 GACAGGGAACGAATGGAGCTCCTGGAGGAAGCTAAGAAGATGGAGATGGC
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Gaps: 26
Percent Identity: 34.074
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                                                                                                                                                                                          Claim 1; Page 216-218; 352pp; English
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1.969
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US-09-445-223-1 x C99717
2001-007495/01
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                              P-PSDB; B55958
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173 513	tSerLeuSerGlnSerArgSerSerLysSerAlaProGluGlyG 	188 550
188	JThrileileTyrMetProProGluAsnTyrGluProGlyGlnLysSer 	204 594
205	ArgalaSerIleLysHisAspIleTyrSerTyrAlaValIleThrTr 	220 . 644
220	pGluValLeuSerArgLysGlnPrOPheGluAspValThrAsnProLeuG 	237 694
237 595	uGlu GAG	253 732
254 733	SerLeuproTyrAspileProHisArgAlaArgMetileSe 2	267 . 782
267	77 rLeuileGluSerGlyFrpAlaGlnAsnProAspGluArgProSerPheL 2 :	284 825
284 326	euLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGluIle 3	300 840
	ThrPheLeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSerVa 3	317
341		843
317	SLeuCysaspLysLysMetGluLeuSerLeuA	334 888
334 389	snileProValAsnHisGlyProGlnGluGluSerCysGlySerSerGln:::	350 933
351 934	uHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPris:	367 983
367	laGlnAspCysTyrPheMet ::: CCGAGTTGC	383 1015
384)16	LysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGl	400 1035
001	ySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSerA 	417
117	hralaglyAsnSerGluArgLeuGlnPro	1105
134	GTGTCCTCAGTGGACCACTTTCC	444 1155
144	gGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuA	61
161	spalaLeuLeuSerArqAspLeuIleMetLvsGluAspTvrGluLeuVal	11/2

1173 ACGINTTYTOLOGY 1184 ATT SETTHILYTOLOGY 1187 ACGICTTYTOLOGY 1187 ACGICTTYTOLOGY 1187 ACGICTTYTOLOGY 1187 ACGICTTYTOLOGY 1187 ACGICTTYTOLOGY 1187 ACGICTTYTOLOGY 1188 THE PROPERTY SETTHING ACGIC
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ខូខូខូ	N-terminal signal sequence, indicating that the proteins are secreted. Sequences 261650-261668, 261766-261780, 261812-261817 and 261827-261829 encode proteins with one or more putative transmembrane domains.
X O	Sequence 1774 BP; 406 A; 490 C; 526 G; 352 T; 0 other;
alig	<pre>gnment_scores:</pre>
alig	mment_brack_07 00-445,-203-1 x Z61830
A11	1/1 to: 2618
	10 LeuProThrileProTyrHisLysLeuAlaAspLeuArgTyrLeuSerAr 26
	26 gGlyalaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValG 43 ::: ::::: ::: 95 GGGGGGTTCGGGCAGGTGTACAAGGTGCCCATGTACATGGAAGACGT 144
	43 lnvalAlavalLysHisLeuHisIleHisThrProLeuLeu 56 :::
	57 AspSerGluargLysAspValLeuargGluAlaGluIleLeuHisLysAl 73
	73 aargpheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGluP 90
	90 heLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluLeu 106 ::: ::: :::
	107 LeuhisArgLysThrGluTyrProAspValAlaTrpProLeuArgPheAr 123 ::: 327 CTGGCCTCAGAGCCATTGCCTTGGGACCTGCGCTTTCG 364
	123 gIleLeuHisGlulleAlaLeuGlyValAsnTyrLeuHisAsnMetThrP 140
	140 roproLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsn 156
	157 GluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMetWe 173 ::::::
	188 lythrileiletyrmetProProGludsnfyrGluProGlyGlnLysSer 204
	205 ArgalaSerIleLysHisAspIleTyrSerTyralaValIleThrTr 220
	220 pgluValLeuSerArgLysGlnPrOPheGluAspValThrAsnProLeuG 237

527 erArgSerProSerLeu 532

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present polynucleotide encodes a polypeptide which is expressed in mammalian skin cells. The polypeptide is useful for stimulating keratinocyte growth and motility, inhibiting the growth of cancer cells, modulating angiogenesis, inhibiting angiogenesis and vascularisation of tumours, modulating skin inflammation, stimulating the growth of epithelial cells, inhibiting the binding of human immunodeficiency virus (HIV) 1 to leukocytes, and treating inflammatory disease, cancer and neurological diseases. The polynucleotide can be used as a marker, in the identification of genetic disorders, and for the design of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide used in the identification of genetic disorders and encoding polypeptides used for treating inflammatory disease, cancer and neurological diseases -
                                                                                                                                                                                                                                                                                                                                                         nootropic; neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; angiogenesis inhibition; inflammation; neurological disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kumble KD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |||::: ||| ::::|||| ::::::||||||::::
                                                                                                                                                                                                                                                                                                                                   Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV;
                                                                 seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA2001.DAT:C99763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10 LeuProThrIleProTyrHisLysLeuAlaAspLeuArgTyrLeuSerAr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 gGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1774 BP; 406 A; 490 C; 526 G; 352 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oligonucleotides for examining expression patterns.
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Gaps: 26
Percent Identity: 33.889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Onrust R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GENE-) GENESIS RES & DEV CORP
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                                                                                                                                                                                                                                                                                   Skin cell cDNA, SEQ ID NO: 403.
                                                                                                                                          ВР
                                                                                                               seq_documentation_block:
ID C99763 standard; cDNA; 1774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-MAY-2000; 2000WO-NZ00075
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08-MAR-2001 (first entry)
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1.963
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US-09-445-223-1 x C99763
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P-PSDB; B56062.
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200069884-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1
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326
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                                                                                                                                                                                                                                                                                                                                                                                          327 CTGGCCTCAGAG......CCATTGCCTTGGGACCTGCGCTTTCG 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 roProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsn 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                647 GGGTGTGCTTACACAGAAGAAGCCATTTGCAGATGAAAAGAACATCCTAC 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 InIleMetTyrSerValSerGlnGlyHisArgProValIleAsnGluGlu 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .TCTGAAACAGAAGACCTTTGTGAGAAGCCTGATGAGGAGGTGAAA.... 890
                                                             73
                                                                                                                                                                                                                                                                                183 GACAGGGAACGAATGGAGCTCCTGGAGGAAGCTAAGAAGATGGAGATGGC
                                                                                                                                                         73 aArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGluP
                                                                                                                                                                                                                                                                                                                                                                                                                                         123 gIleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetThrP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMetMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           465 CACTACCATGTCAAGATTTCTGACTTTGGGCTGGCCAAGTGCAATGGCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tSerLeuSerGlnSerArgSerSerLysSerAlaProGluGly.....G
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735 CTGCCCACCCATCTGCAGACCCCGGCCGTGCCTGTGCCAGCCTGATAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 euLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGluIle
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                                                                                                                                                                                    233 CAAGTTCCGATACATTCTACCTGTATAGCGGGATATGCCAGGAACCT....
                                                                                                                                                                                                                                                    heLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluLeu
                                                                                                                                                                                                                                                                                                                                                LeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPheAr
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                                                                AspSerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLysAl
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256 resecreases.....ccarrecerreseacerecerrese 293
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                                                                                                           (IMMV ) IMMUNEX CORP
                                                                                                                                           Virca GD, Bird TA,
                                                                                                                                                                           WPI; 2000-205722/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                           P-PSDB; Y79154.
                                                           04-AUĞ-1998;
11-SEP-1998;
                               04-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores
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17-FEB-2000
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 1188
                                                                                                                                                                                                                                                                                       1038 ATCTCCCAGACTCTTG........AAGGCCCCGAAGAGCTCAG 1072
                                                                                                                                                                                                                                                                                                                                            1218 ACAGACATCCAGAAGAAGCAGCTAGTGGATGCCATCATATCAGGGGACAC 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1268 CAGCAGGCTGATGAAGATCCTACAGCCCCAAGATGTGGACTTGGTTCTAG 1317
                                                                                                                                                                                                                                                                                                                                                                                                                   GCAGTGGCAAGAGGCTCTCGGGGGTGTCCTCAGTGGACTCAGCCTTTTCC 1157
                                                                                                                                                                                           400
                                                                                                                                                                                                                                                                                                                        417 laIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnPro 433
                                                                                                                                                                                                                                                                                                                                                                                                                                               444 gGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuA 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           461 spAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeuVal 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478 SerThrLysProThrArgThrSerLysValArgGlnLeu..LeuAspThr 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    510 sAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValValS 527
   334 snileProValAsnHisGlyProGlnGluGluSerCysGlySerSerGln 350
                                                                                                                              oGlnAspAsnAsp.PheLeuSerArgLysAlaGlnAspCysTyrPheMet 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA2000.DAT:258584
                                                                                                                                                                                                                           1018 ......rgr....cacaGrrgG.....acrcrggg
                                                                                                                                                                                                                                                                                                                                                                                     434 GlyIleAlaGln.....GlnTrpIleGlnSerLysAr
                               ....GACCTGGCTCATGAGCCAGGCGAGAAAGCTCTCTAGAGTCCAAG
                                                                351 LeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPr
                                                                                   986 CTTCGATAACGACTGCAGTCTCT.....CCGAGTTGC.....
                                                                                                                                                                                           LysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGl
                                                                                                                                                                                                                                                            400 ySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSerA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     494 ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fel; protein kinase; mouse; signal transduction; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1158 TCCAGAG.....GATCGCTGT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 3..2294
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ID 258584 standard; cDNA; 2294 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUN-2000 (first entry)
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527

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The present sequence is that of Genesis clone 971025TRAM004820HT (Fel) DNA. The translation of the clone (frame 3) is provided in 779134. The propertied has kinase activity. The invention cry9134. The purified murine polypeptides (see Y79152-56) that relates to purified murine polypeptides (see Y79152-56) that have kinase function and isolated nucleic acids encoding them (see COTYPEPERSON OF THE NUCLEIC acids encoding them (see DOTYPEPERSON OF THE NUCLEIC acids encoding proteins polypeptides, as probes to identify nucleic acids encoding proteins having kinase activity, and in assays to identify chromosomes; map nucleic acids and host cells (bacterial, yeast, plant, insect or animal) transfected or transduced with the vectors are claimed. The kinase polypeptides and their fragments are used as mol.wt. and isoelectric focusing markers, and as controls for peptide fragmentation. They also have a number of therapeutic uses, as kinases play a central role in cellular signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                            Novel murine polynucleotides encoding kinase polypeptides, used a probes to identify nucleic acids encoding proteins having kinase activity -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPheArg 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112 ACAGGGAACGAATGGAGCTCCTGGAGGAAGCTAAGAAGATGGAGATGGCC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluLeuL 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 GCTCGCGATCAAGTGCTCGCCCAGTCTGCACGTCGAC.........G 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 spSerGluargLysAspValLeuArgGluAlaGluIleLeuHisLysAla 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 GCCGCTTCGGCCAGGTGTACAAGGTGCGCCATGTGCACGTG 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 GlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2294 BP; 526 A; 639 C; 666 G; 463 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 523
Gaps: 26
Percent Identity: 34.608
                                                                                                                                                                                                                                             Anderson DM, 'Marken JS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Fig 3; 93pp; English
99WO-US17577
                                                                    98US-0095269
98US-0099973
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140 343	157 393	173	188	205	220 575	237	254 663	267	284	301	Ξ.		334	351	367	384 945	400	417	434
124 IleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetThrPr ::: ::: :::	140 oProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsnG 	157 luPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMetMet ::::	174 SerLeuserGlnserArgserSerLysserAlaProGluGlyGl	nTy : AAT	205 rgAlaSerIleLysHisAspIleTyrSerTyrAlaValIleThrTrp 	221 GluValLeuSerArgLysGlnProPheGluAspValThrAsnProLeuGl ::::: :::	237 nIleMetTyrSerValSerGlnGlyHisArgProValIleAsnGluGluS :	254 erLeuproTyraspileproHisargAlaargMetileSer 	268 LeulleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerPheLe	II-	01 hrPheLeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSerVa 	72 cc	318 SerSerAlalleHisLeuCysAspLysLysLysMetGluLeuSerLeuAs	334 nlleProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnL :::	351 euHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPro 111	368 Glnaspasnasp.PheLeuSerargLysalaGlnaspCysTyrPheMetL ::: 915 TTCGATAACGACTGCAGTCTCTCCGAGTTGC	384 ysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGly	401 SerGlnargalaalaPheCysaspHisLysThrThrProCysSerSeral 	417 allelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGlnProG

478 erThrLysProThrArgPhrsertysyalArgGlnLeu. LeukspThrT 494 1117
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.. GlyThrIleIleTyrMetProProGluAsnTyrGluProGlyGlnLys

dermal papilla, human keratinocytes and neonatal foreskin fibroblasts, and mouse embryonic skin, keratinocyte stem cells and transit amplifying cells. Polypeptides of the invention may be used to treat inflammation, cancer and neurological diseases. The proteins may be used to stimulate the growth and motility of keratinocytes, to inhibit the growth of cancer cells, to modulate anglogenesis and tumour vascularisation, to modulate skin inflammation, to modulate epithelial cell growth and to inhibit binding of HIV-1 to leukocytes. The invention may also be used to treat growth and developmental defects, skin wounds and hair follicle disorders. Sequences 261606-261832 represent conka sequences derived from several mouse, rat or human skin cell types. Sequences 261606-26181 and 261826 encode proteins with an N-terminal signal sequence, indicating that the proteins are secreted. Sequences 261600-26168, 261780, 261812-26181 and 261827-261829 encode proteins with one or more putative transmembrane domains. Sequence 1888 BP; 433 A; 518 C; 554 G; 380 T; 3 other;

Length: 541 Gaps: 27 Percent Identity: 33.272 548.00 1.845 54.898 US-09-445-223-1 x Z61671 Quality: Ratio: Percent Similarity: alignment_scores alignment_block:

to: 1888 from: 1 Align seg 1/1 to: 261671

90 heLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluLeu 106 93 GGCCGCTTCGGGCAGGTGTACAAGGTGCGCCATGTGCACTGGAAGACGT 142 43 CTGCGCACCTTCGACGCCGGCGAATTCGCAGGCTGGGAGAAGGTGGGCTC 92 gGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValG LeuProThrIleProTyrHisLysLeuAlaAspLeuArgTyrLeuSerAr 143 GGCTCGCGATCAAGTGCTCGCCCAGTCTGCACGTCGAC....... AspSerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLysAl GACAGGGAACGAATGGAGCTCCTGGAGGAAGCTAAGAAGATGGAGATGGC aArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGluP 10 56 22 181 73

277

glleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetThrP 140 LeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPheArccaltgccltggaccrgcgctrfcg CTGGCCTCAGAG. 325 123 107

roProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsn 156 363 CATCGTGCACGAGACAGCCGTGGGCATGAACTTCCTGCATTGCATGTCTC GGCCACTGCTGCACCTGAAGCCAGCGAACATCTTGCTGGATGCC 140 413

GluPheHisVal...LysIleAlaAspPheGlyLeuSerLysTrpArgMe 172 CACTACCAAATGTCAAGATTTCTTGACTTTGGGCTGGCCAAGTGCAATGG 463 157

tMetSerLeuSerGlnSerArgSerSerLysSerAlaProGluGly.... 187

172

477 ValSerThrLysProThrArgThrSerLysValArgGlnLeu..LeuAsp 492

........CACAGITGG.....ACTCTGGG 1038 .039 ATCTTCCCAA......GACTCTTGAAAGGCCCCGAAGAGCT 1073 rGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerS 416 sArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerL 460 783 AGGCCTCATGCAACGGTGCTGCATGCAGACCCACAGGGGCCC.... 828 840 349 MetLysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSe 399 eralailelleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432 euAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeu 476GACCTGGCTCATGAGCCAGGAGAAAAGCTCTTAGAGTCC 933 GlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAl 366 aProGlnAspAsnAsp.PheLeuSerArgLysAlaGlnAspCysTyrPhe 382 GluSerLeuProTyrAspIleProH1sArg......AlaArgMetIl 266 heLeuLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGlu 299 300 IleThrPheLeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSe 316 316 rValSerSerAlaIleHisLeuCysAspLysLysMetGluLeuSerL 333TCTGAAACAGAAGACCTTTGTGAGAAGCCTGATGAGGAGGTGAAA. 891GAGAAG 934 AAGAGTGAGGCCAGGCCCGAGTCCTCACGCCTCAAGCGCGCCTCTGCTCC euGlnIleMetTyrSerValSerGlnGlyHisArgProValIleAsnGlu ||:::|||||| TACACATCATGATGAAAGTGGTAAAGGGCCACCGCCCA......ACCTTCCAAGAA SerArgAla...SerIleLysHisAspileTyrSerTyrAlaValileTh 645 CTGGGGTGTGCTTACACAGAATAATCCATTTGCAGATGAAAAAACATCC 733 GAGCTGCCACCCATCTGCAGACCCCGGCCGCGTGCCTGTGCCAGCCTGAT eSerLeuIleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerP rTrpGluValLeuSerArgLysGlnProPheGluAspValThrAsnProL euAsnIleProValAsnHisGlyProGlnGluGluGluSerCysGlySerSer ProGly11eAlaGln.....GlnTrpIleGlnSerLy 551 TTGGTACAATCGGCTACCTCCCTCCAGAGCGAATTCGT 1159 TCCTCCAGAG.....GATCGCTGT TDL....TGL . CACTGTCTTTTGAGC ATTACC 204 595 253 829 847 383 399 416 433 460 219 236 695 266 283 333 892 443

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from: 1

to: C99604

Align seg 1/1

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alignment_block:
US-09-445-223-1 x C99604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murison JG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse; skin cell; cytostatic; antiinflammatory; anti-HIV; mootropic; neuroprotective; vulnerary; immunomodulatory; vaccine; keratinocyte growth stimulation; cancer; anglogenesis inhibition; inflammation; neurological disease; ss.
                                1269 CACCAGCAGGCTGATGAAGATCCTACAGCCCCAAGATGTGGACTTGGTTC 1318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KD,
                                                                                                                                                     1219 CCCACAGACATCCAGAAGAAGAAGCTAGTGGATGCCATCATATCAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn1_8/gcgdata/geneseq/geneseqn/NA2001.DAT:C99604
                                                                                                                                                                                                                                     509 uLysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValV
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                                                                                                  493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sleeman M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 109-110; 352pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Onrust R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GENE-) GENESIS RES & DEV CORP LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C99604 standard; cDNA; 1888 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 1319 TAGACAGCAGTGCCAGCCTG 1338
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Length: 541 Gaps: 27 Percent Identity: 33.272

548.00 1.845 54.898

Quality:
Ratio:
Percent Similarity:

alignment_scores:

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324
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                                                                                                                                                                                                                                                                                                                                               90 heLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluLeu 106
                                                                                                                                                                                                                                                                                                                                                                                                                 LeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPheAr 123
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                                                                                                                                                                                                                                                                           73 aArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGluP 90
                              43 CTGCGCACCTTCGACGCCGGCGAATTCGCAGGCTGGGAAGGTGGGCTC 92
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..GTCGGCTTGGTCATGGAGTACATGGAGAACAGGCTCCCTGGAGAAGCTG
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10 LeuProThrIleProTyrHisLysLeuAlaAspLeuArgTyrLeuSerAr
                                                                   26 gGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValG
                                                                                                                                   tMetSerLeuSerGlnSerArgSerSerLysSerAlaProGluGly....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ..GlyThrIleIleTyrMetProProGluAsnTyrGluProGlyGlnLys
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ......TGT.....CACAGTTGG....ACTCTGGG 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1109 CCAGCAGTGGCAAGAGGCTCTCGGGGGTGTCCTCAGTGGACTCAGCCTTT 1158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .....GGGAAGCTTCAACAGGCGACCTGGGC 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493 ThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLe 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         383 MetLysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSe 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rGlySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerS 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   erAlaIleIleAsnProLeuSerThrAlaGlyAsnSerGluArgLeuGln 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          443 sArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerL 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       euAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrGluLeu 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       477 ValSerThrLysProThrArgThrSerLysValArgGlnLeu..LeuAsp 492
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aProGlnAspAsnAsp.PheLeuSerArgLysAlaGlnAspCysTyrPhe 382
283 heLeuLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGlu 299
                                          .....ACCTTCCAAGAA 840
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                                                                                                                                                                                                                                                                                    333 euAsnIleProValAsnHisGlyProGlnGluGluSerCysGlySerSer
                                                                                                                                                                                                                                                                                                                .::....AATGCAAGCTCCCATCGT
                                                                                          300 IleThrPheLeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSe
                                                                                                                                                                                       316 rValSerSerAlaIleHisLeuCysAspLysLysLysMetGluLeuSerL
                                                                                                                                                                                                                                    847 ....TCTGAAACAGAGCCTTTGTGAGAAGCCTGATGAGGGGGGTGAAA.
                                                                                                                                                                                                                                                                                                                                                                               350 GlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAl
                                                                                                                                                                                                                                                                                                                                                                                                                              934 AAGAGTGAGGCCAGGCCCGAGTCCTCACGCCTCAAGCGCGCCTCTGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1039 ATCTTCCCAA.....GACTCTTGAAAGGCCCCGAAGAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ProGly11eAlaGln............GlnTrpIleGlnSerLy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1178 ..cacrgrctrtrgagc.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВР
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                526 alSerArgSerProSerLeu 532
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ID T43752 standard; cDNA; 2268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 841 ATTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T43752,
                                             829
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              366
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(first entry)

13-FEB-1997

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- useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A cDNA clone (T43752) codes for mouse receptor interacting protein (RIP) (W04627), a protein which contains a C-terminal death domain through which RIP interacts with the Fas/APO-1 intracellular domain (ICD). RIP overexpression leads to cell death. The RIP cDNA was identified from a mouse thymus cDNA library by screening with the human RIP coding sequence (see also T43753) and sequence analysis of overlapping clones. It can be used as a probe and to produce recombinant RIP in host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor interacting protein having death and kinase domain to control diseases that involve abnormal apoptosis, and for diagnosis and drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 uPheLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluL 106 ::::::||| |||||||||| ::::||| ::::|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 CTGAGACACAGTCGAGTGAAGCTACTGGGGCATCATCATAGAAGAAGG 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            168 IGGATTIGICATCCIGAAAAA......GIATACACAGGGCCCAACC 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 GCCTGAGTACAATGAGGTTCTCTTGGAAGAGGGGAAGATGATGCACAGA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57
                             Receptor interacting protein; RIP; cell death; apoptosis; Fas; APO-1; signal transduction; cancer; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 LeuSerArgGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTr 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            57 spSerGluArgLysAspVal...LeuArgGluAlaGluIleLeuHisLys 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73 AlaArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGl 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 pargvalGlnvalAlavalLysHisLeuHisIleHisThrProLeuLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2268 BP; 719 A; 491 C; 576 G; 482 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 609
Gaps): 25
Percent Identity: 25.452
                                                                                                                                                                                                                                                                                                                                                                  Stranger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 2268
Mouse receptor interacting protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 38-39; 64pp; English.
                                                                                                            Location/Qualifiers
52..2022
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: T43752 from: 1
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51.232
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US-09-445-223-1 x T43752
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; W04627
                                                                                                                                                                                                                                                18-APR-1996;
                                                                                                                                                                                                                                                                               18-MAY-1995;
                                                                                                                                                                                 WO9636730-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                21-NOV-1996
                                                                                  Mus sp
                                                                                                                Key
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111	309 359	35	
PROPROIGEULGHHISHISASPLEULYSTHYGINASNIIGEULGUARDA 156 AAAGGTGTGATACACAGGACCTGAAGCTGAAGAATATCTCGTCGTTGGT SNGIUPHEHISVALLYSILAALASPHAGCTGAAGAATATCTCGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT	23	3	
snGluPheHisValLyslleAlaAspPheGlyLeuSerLysTrpArgMet 172 """::!	39 45	15	
MetSerLeuserGlnSerkgserSerlysSeralapro 185	56 94	17 54	
CACCACTAAGAAGAATGGTAGCCTTTACTACATGGCACCGAAC 643	73	18 AG 59	
LysHisaxpileTyrSerTyralavalileTheyserArgalaserile 208 ACCTGAARGCCAAGGGGAGGAAGTCG	94	19	
LyshishspileTyrSerTyralaValileThrTrpGluValLeuSerAr 225	97	a) ·	
glysGlnProPheGluAspValThrAsnProLeuGlnIleMetTyrServ 242	92	SASPILGTYrSerTyralaVallleThrTrpGluValLeuSerar 22 ::: :::::::::: GACGTGTACAGCTTTGGCATTGTCCTTTGGGCAATATTTGCAAA 72	
alSerGinGlyHisArgProvalileAsnGluGluSerLeuPro 256 ::::::: :::	25	24	
TyrAspileProHisArgAlaArgMetileSerLeuileGluSerGlyTr 273 :: AGGGGATCATCAGCCTCATGGAGGGGTGCTG 857 palaGlnAsnProAspGluArgProSerPheLeuLysCysLeuileGluL 290	12	25	
PalaGlnAsnProAspGluArgProSerPheLeuLysCysLeuIleGluL 290	57	27	
euGluProValLeuArgThrPheGluGluIleThrPheLeuGluAla 305 :::: TTAGGCCTTTTAACTCATTTTGAAGAAAATATGTAGAAGAGGT 954 ValIleGlnLeuLySLySThrLysLeuGlnSe 316	73		
ValileGinLeuLysLys	90		
1	96	316	
AsplysLysLysMetGluLeuSerLeuAsnileProValAsnHisGly 340	16 35	324	
ProGlnGluGluGerCysGlySerSerGlnLeuHisGl 353	25		
uAsnSerGlySerProGluThr360	11		
CERCE RECOVER CONTRACTOR AND CONTRAC	6 4	uAsnSerGlySerProGluThr	

1.,	361SerArgSerLeuProAlaProGlnAspAsn	370
17	1205 CTTTTGGAATATTGCAGAGAACAGACAAAACGGCAGCCAGGCAAGGCAGAAAT	1254
.,	371 AspPheLeuSerArgLysAlaGlnAspCysTyrPheMetLysLeuHisHi	387
77	1255 GAGGCTTACAACAGAGGAGGAGAGGAAACGAAGGGTCTCTCA	1298
(*)	387 sCyspro	389
17	1299 TGACCCCTTTGCACAGCAGAGCTCGTGAGAATATTAAGAGTGCAGGAG	1348
(*)	390GlyAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAla	405
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4 ,	406 PheCysAspHisLysThrThrProCysSerAlallelleAsn	420
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14	1490 CGCCAAATCTAAGCCAAATGTATAGTACTTATAAAACTCCAGTGCCAGAG	1539
4	443	443
1.5	1540 ACCAACATACCGGGAAGCACCACCATGCCATACTTCTCTGGGCCAGT	1589
4	444 .ArgGluAspIleVal.AsnGlnMet	451
11	1590 AGCAGATGACCTCATAAAATATACTATATTCAATAGTTCTGGTATTCAGA	1639
4	452 ThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAspLe	468
16	1640 TTGGAAACCACAATTATATGGATGTTGGACTGAATTCACAACCACCAAA	1689
4	468 ulleMetLysGluAspTyrGluLeuValSerThrLysProThrArgThrS	485
16	1690 AATACTTGCAAAGAAGACTCGACTTCCAGACACCCAAGCCATCTTGATA	1739
4	485 erLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGlu	499
17	1740 CACCACTAGTCTGATGAACACCTGAACCTATCAGGGAAACCTG	1789
,	500GlupheAlaLysValIleValGl	507
17	1790 GAAGGCAGIGGAAAAACIGIGCCCGCAAGCIGGGCTICACIGAGTCICAG	1839
u,	507 nLysLeuLysAspAsnLysGlnMet 515	
16	1840 ATCGATGAAATCGACCATGACTATG 1864	

AA301765 EST14819 Aorta endo BE002713 QV4-BN0090-210300-1 8A226052 0660b09.s1 NCI_CGAP BF825562 CMI-HN0016-161100-5

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/db_xref="taxon:9666"
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/clone='IndexE:4426016"
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/tissue_type="hypernephroma, cell line"
/tab_host="Dh10B (phage=resistant)"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sali; cloned unidirectionally; oligo-dT primed.
Average insert size 1.3 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 811)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                   BG170405 811 bp mRNA EST 06-FEB-2001 602322736F1 NIH_MGC_89 Homo sapiens cDNA clone IMAGE:4426016 mRNA sequence.
BG170405 G1:12677108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10172 row: g column: 09
High quality sequence stop: 721.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 AAATCCAGATGAAAGACCATCTTTCTTAAAATGTTTAATAGAACTTGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 270
Gaps: 3
Percent Identity: 94.074
  337
446
400
346
1.5e-48
2.4e-48
5.1e-48
8.2e-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1 to: 811
1034.81
1031.20
1025.27
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572.00
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96.296
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Ratio: 4.933
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US-09-445-223-1 x BG170405
                                                                                                                                         seq_name: gb_est97:BG170405
                                                                                                                                                                                               seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   272
                                                                                                                                                                                                                                                                                                                                                                                           human.
                            gb_est68:BE002713
gb_est12:AA826052
gb_est92:BF825562
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                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
ORGANISM
                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
JOURNAL
COMMENT
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ORIGIN
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AUTHORS
                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                  VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG170405 60232736F1 NIH_MGC_89
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BE551615 AZ4906.x1 NCI_CGAP_GC
AA10113 2058405.s1 Stratagene
AI94799 IL-BT067-190199-023 BI
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BF460494 UI-M-CG0p-bmd-c-04-0-U
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AW593657 x194d07.xl NCI_CGAP_Ut
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AA72233 ag73908.sl Soares_feta
AW465726 BP23002020D3 soares r
A1307810 tb28d07.xl NCI_CGAP_Ki
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BF754627 QV3-CT0558-121000-377
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AW389881 RC4-ST0173-131099-031
                                                                                                                                                                                                             About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <del>_.</del>
  out_format : pfs
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3e-71
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                       pLysLysLysMetGluLeuSerLeuAsnIleProValAsnHisGlyProG 342
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1:1 kb. Library constructed by Life
                Tel: (301) 496-1550
Tel: (301) 496-1550
Email: Robert Strausberg@nih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
Plate: LLAM9609 row: q column: 24
High quality sequence stop: 739.
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Percent Identity: 98.361
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Robert Strausberg, Ph.D.
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Ratio: 4.846
Percent Similarity: 98.770
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Homo sapiens
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to:654)
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BE536247
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Site_2: SalI: Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.1 kb. Library constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tel: (301) 496-1550
Email: Robert Strausbergenih.gov
Tissue Procurement: DCTD/DTP/Gazdar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9669 row: n column: 06
High quality sequence stop: 795.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 828)
1 thtp://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE875947 828 bp mRNA EST 20-OCT-2000 601486423F1 NIH_MGC_69 Homo sapiens cDNA clone IMAGE:3888965 5',
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                                                                                             465 rArgAspLeulleMetLysGluAspTyrGluLeuValSerThrLysProT
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BE875947
BE875947.1 GI:10324723
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163 c
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Ratio: 5.029
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LOCUS
BE875947
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                                                                                                                                                                                                                                                                                                                                                            /note-"Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."
                         National institutes of health, mammatran state contacts. When the contacts Robert Strausberg, Ph.D.
Contacts Robert Strausberg hh.D.
Tals: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
cONA Library Preparation: Life Technologies, Inc.
cONA Library Arrayed by: Incyte Genomics, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
cDNA Library Arrayed by: Constitution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.lln.gov
Plate: LiAM84125 row: o column: 08
High quality sequence stop: 650.
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                Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 sLysMetGluLeuSerLeuAsnIleProValAsnHisGlyProGlnGluG 344
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Percent Identity: 95.890
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
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Percent Similarity: 96.804
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Ratio: 4.807
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US-09-445-223-1 x BE536247
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                TITLE
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 AUTHORS
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 645)

11 (bases 1 to 645)

12 (bissoe, S., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Halller, L., Lennon, G., Becker, M., Favello, A., Gish, M., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, M., Mortis, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA160547 645 bp mRNA EST 16-DEC-1996 zq49c11.rl Stratagene hNr neuron (#937233) Homo sapiens cDNA clone IMAGE:633044 5', mRNA sequence.
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1800
Email: est@Astson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 373.
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/note="Vector: pBluescript"
/note=
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alignment_scores:

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Quality: 940.00
Ratio: 5.193
Percent Similarity: 100.000
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                                                                       TITLE
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LOCUS AI745575 592 bp mRNA EST 17-DEC-1999
DEFINITION wc34f12.x1 NCI_CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2317103 3'
similar to TR:043353 043353 SERINE/THREONINE KINASE RICK. ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rSerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuP 365
                                                                                                                                                                                                                           OValIleAsnGluGluSerLeuProTyrAspIleProHisArgAlaArgM 265
                                                                                                                                                                                                                                            281
                                                                                                                                                                                                                                                                                                               102 TGATCTCTCAAAAGTGGATGGGCACAAAATCCAGATGAAAGACCA 151
                                                                                                                                                                                                                                                                                                                                                               SerPheLeuLysCysLeuIleGluLeuGluProValLeuArgThrPheGl 298
                                                                                                                                                                                                                                                                                                                                                                                                TCTTTCTTAAAATGTTTAATAGAACTTGAACCAGTTTTGAGAACATTTGA
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                                Percent Identity: 92.891
                   Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlnProGlyIleAlaGlnGlnTrpIleGlnSer 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     598 CAGCCT...GTATGCCCGCAGTGGATCCGAGCA 627
                                                                                                                      from: 1
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AI745575.1 GI:5113863
995.00
4.901
96.209
                                                                                                                      Align seg 1/1 to: AA160647
                                                                                      US-09-445-223-1 x AA160647
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
   Quality:
                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
                   Ratio:
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                                                                      alignment block:
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VERSION
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SOURCE
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/note="Organ: prostate; Vector: pT713D-Pac (Pharmacia)
with a modified polylinker: Plasmid DNA from the
normalized library NCI_CGAP_P122 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986739, 1101192-1101959, and 1217928-1220615).
Subtraction bento Soares and M. Fatima Bonaldo. "
11 c 128 g 200 t
                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing Center
information can be
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo. 1 (bases 1 to 592)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                             Ph.D., Michael
                                                                                                                                                                                                                                                                                    Tissue Producement: Michael J. Brownstein, M.D., Ph. Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Preparation: M. Bento Soares, Ph.D. DNA Sequencing by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sec Clone distribution: NCI-cGAP clone distribution in Cound through the I.M.A.G.E. Consortium/Link at: www-bio.lnl.gov/bbp/image/image.html
Insert Length: 673 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 ThrSerArgSerLeuProAlaProGlnAspAsnAspPheLeuSerArgLy 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          376 sAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisS 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        393 erTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheCysAspHis 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              410 LysThrThrProCysSerSerAlaIleIleAsnProLeuSerThrAlaGl 426
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Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:2317103"
/clone_11b="NCI_CGAP_Pr28"
                                                                                                                                          Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens'
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 459.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="male"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to reverse of: AI745575
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US-09-445-223-1 x AI745575/rev
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534 TGCCAGAATTTCGGCACGAGGAAAAATAGTGGTTCTCTTAAAATTTCAAG
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TITLE
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dasea 1 to 647) Hegde, P., 01/R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, J.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
LOCUS AM$60501 647 bp mRNA EST 01-JUN-2000
DEFINITION EST372572 MAGE resequences, MAGF Homo sapiens CDNA, mRNA sequence.
ACCESSION AW$60501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     colon tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assessment of gene expression patterns in a model of metastasis using a 19,200 element CDNA microarray Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research 9112 Medical Center Dr., Rockville, MD 20850, USA Par: 301 838 3528
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 CysGlySerSerGlnLeuHisGluAsnSerGlySerProGluThrSerAr 362
                                                              192 CTACTGACATCCAAGGAGAAGAATTTGCCAAAGTTATAGTACAAAATTG 143
                                                                                                                                                                                                                                                            526
                                                                                                                              493
                                                                                                                                               uValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspT
                                                                                                                                                                                             493 hrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 647
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Percent Identity: 92.857
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1. 647
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a 128 c 141 g 213 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: johnq@tigr.org
Plate: 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-445-223-1 x AW960501/rev
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4.930
94.898
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Percent Similarity:
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ORIGIN
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VERSION
KEYWORDS
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                                                                                                                                476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
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Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
CDNA_Library Preparation: M. Bento Soares, Ph.D., M. Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BES51615 636 bp mRNA EST 10-AUG-2000 7442906.x1 NCI_CGAP_GC6 Homo sapiens CDNA clone IMAGE:3221434 3' similar to TR:043353 043353 SERINE/THREONINE KINASE RICK. ; mRNA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Mammaliai; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 636)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap:
National Cancer Institute, Cancer Genome Anatomy Project (GGAP),
                                                                                                                                                                                                                                                                                          412
                                                                                                                                                                   428
                                                                                                                                                                                                                                                          385
                                                                                                                                                                                                                                                                                                                                                                   462
                                                                                                                                                                                                                                                                                                                                                                                                      334 AGACATTGTGAACCAAATGACAGAAGCCTGCCTTAACCAGTCGCTAGATG 285
                                                                                                                                                                                                                                                                                                                                                                                                                                            478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               235
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                                                                     379 AspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSerTrpAs 395
                                                                                          535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 ACAAACAAATGGGTCTTCAGCCTTACCCGGAAATACTTGTGGTTTCTAGA 85
pSerThrIleSerGlySerGlnArgAlaAlaPheCysAspH1sLysThrT
                                                                                                                                                                                                                       hrProCysSerSerAlallelleAsnProLeuSerThrAlaGlyAsnSer
                                                                                                                                                                                                                                      uAspileValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuAspA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_est75:BE551615
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LOCUS BE551615
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polylinker; plasmid DNA from the normalized library
NOI_CGAP_GC4 was prepared, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive phybridization reaction. The driver
was PCR-amplified cDNAs from a pool of 5,000 clones made
from the same library (cloneIDs 1257096-1258631,
1469064-1470983, and 145592-1476743). Subtraction by
Bento Soares and M. Fatima Bonaldo. " subtraction by
DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov Seq primer: -40UP from Gibco High quality sequence stop: 455.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             376 sAlaGlnAspCysTyrPheMetLysLeuHisHisCysProGlyAsnHisS 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysThrThrProCysSerSerAlaIleIleAsnProLeuSerThrAlaG1 426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspT 493
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Percent Identity: 98.343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-445-223-1 x BE551615/rev
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                                                                                                                      FEATURES
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Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 568)

1 (hases 1 to 568)

2 (hases 1 to 568)

3 (hases 1 to 568)

3 (hases 1 to 568)

4 (hases 1 to 568)

4
                                                                                                                                                                                                                                                                                                                                                                  ZO58405.s1 Stratagene pancreas (#937208) Homo sapiens cDNA clone IMAGE:591081 3', mRNA sequence.
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
INSET Length: 1942 Std Error: 0.00
Seq primer: -40M13 fwd. from Amersham
High quality sequence stop: 256.
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/organism="Homo sapiens"
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/sex="female"
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1 (bases 1 to 762)

Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/seq/gethtml.pl?tl=LL&t2=IL-BT067-023.html &t3=190199&t4=1)
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Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010,
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                           sLysThrThrProCysSerSerAlaIleIleAsnProLeuSerThrAlaG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI904799.1 GI:6495186
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Fax: +55-11-2707001
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/dev_stage="Adult"
//dev_stage="Adult"
//note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A minl-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
//16 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        291
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                                                     /organism="Homo sapiens"
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157 c 137 g
                                                                           /db_xref="taxon:9606"
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Location/Qualifiers
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seq_documentation_block:

LOCUS AW085560 606 bp mRNA EST 09-MAR-2000

DEFINITION Wy67-04.x1 Soares_NSF_FRB_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:2553606 3' similar to TR:043353 043353 SERINE/THREONINE

KINASE RICK: ;, mRNA sequence.
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                                                                                                                                   276 CCGCCCGCCACGCAGACTGGCGCGTCCAGGTGGCCGTGAAGCACCTGCAC 325
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                                                                                                             eralaargHisAlaaspTrpArgValGlnValAlaValLysHisLeuHis 50
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                                                               226 ACTCGCCGACCTGCGCTACCTGAGCCGCGCGCCTCTGGCACTGTGTCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  472 AATATCTTATTGGACAATGAATTTCATGTTAAGATTGCAGA.TTTGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          326 ATCCACACTCCGCTGCTCGACAG...............
                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 GlySerLeuAsnGluLeuLeuHisArgLysThrGluTyrProAspValAl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_est41:AW085560
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                      17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 917)

S NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

LOUDLISHed (1999)

Contact: Robert Strausberg, Ph.D.

Tel: (301) 496-1550

Email: Robert_Strausbergenih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at: image.linl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BE274455 917 bp mRNA EST 13-JUL-2000 601120495F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:2967359
                                                                                                               408 spHisLysThrThrProCysSerSerAlaIleIleAsnProLeuSerThr 424
                                                                                    425 AlaGlyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGl 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MetAsnGlyGluAlaIleCysSerAlaLeuProThrIleProTyrHisLy 17
                         Length: 269
Gaps: 5
Percent Identity: 69.888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 734 Location/Qualifiers
                                                                                                                                                                          441 nSerLysArgGluAspIleValAsnGln 450
                                                                                                                                                                                                                 649 AAGCNAAAGGGAAAANTTTGGAACCAA 676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: BE274455 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                             BE274455.1 GI:9149397
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4.284
73.978
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US-09-445-223-1 x BE274455
                                                                                                                                                                                                                                                          seq_name: gb_est72:BE274455
                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BE274455
                                                                                                                                                                                                                                                                                                     seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    193
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                                                                                                                                                                                                                                                                                                                                                DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
TITLE
JOURNAL
COMMENT
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FEATURES

ORIGIN

520

167

117

ACCESSION VERSION KEYWORDS SOURCE

REFERENCE

67

421

FEATURES

TITLE

SOURCE

COMMENT

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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Euteneria; Primates; Catarrhini; Hominidae; Homo.

I Chases I to 484)

Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A., Bult

C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D., White, O., Sutton, G. Blake, J.A., Brandon, R.C., Man-Wal, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fritchman, J.L., Geoghagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., J.T., Kelley, J.M., Moreno-Palaquees, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Beng, D.F., Ferrice, A., Fischer, C., Hastings, G.A., He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Veiterial association of human cane diversity and expression patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence Nature 377 (6547 Suppl), 3-174 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: arkerlar@tigr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi.hfml)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seg_documentation_block:
LOCUS AA315575 484 bp mRNA EST 19-APR-1997
DEFINITION EST187344 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               525
475
                                                                                                                                                                     356 cectacareccerrererecasesacrrrsarcarsaassacrarsa 307
                                                                                                                                                                                                                                         475 uLeuValSerThrLysProThrArgThrSerLysValArgGlnLeuLeuA 492
                                                                                                                                                                                                                                                                                                             257
                                                                                                                                                                                                                                                                                                                                                                              492 spThrThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLys 508
                                                                                                                                                                                                                                                                                                                                                                                                              206 TIGAAAGATAACAAACAAATGGGTCTICAGCCTTACCCGGAAATACTIGT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
                                                                                                                                                                                                                                                                             LeuLysAspAsnLysGlnMetGlyLeuGlnProTyrProGluIleLeuVa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    erLeuAspAlaLeuLeuSerArgAsp.LeuIleMetLysGluAspTyrGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA315575.1 GI:1967904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other_ESTs: THC188294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           end, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_est5:AA315575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96026280
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COMMENT
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AUTHORS
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KEYWORDS
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                                           901
                                                                                                               159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          // Alachingster incoled, Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not 1; Site_2: Eco RI; Equal amounts of plasmid DNA from five normalized libraries were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 5 libraries. The pools consisted of the following libraries and cloneDDs: Soares NBAFF pool 1: 309384-310919, 323208-325895 Soares NBAFF pool 1: 758280-760583, 772104-774407 Soares NBPRA pool 1: 758280-760583, 772104-774407 Soares NBHPA pool 1: 758280-760583, 77210407 Soares NBHPA pool 1: 772990-774407 Soares NBHPA pool 1: 77204-774407 Soares N
                                                                                                                          Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 606)

1 (bases 1 to 606)

NOT-GGAP http://www.ncbi.nlm.nih.gov/nclcgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550

Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@lmage.llnl.gov) for further information.
Insert Length: 885 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 470.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    isLysThrThrProCysSerSerAlaIleIleAsnProLeuSerThrAla 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         506 ACAAGACCACTCCATGCTCTTCAGCAATAATAAATCCACTCTCAACTGCA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          426 GlyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIleGlnSe 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 442 rLysArgGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnS 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="TWAGE: 2553606"
/clone_11b="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to reverse of: AW085560 from: 1 to: 606
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Percent Identity: 98.795
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    .606
    /organism="Homo sapiens"
/db_xref="taxon:9606"

                 AW085560.1 GI:6040712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-445-223-1 x AW085560/rev
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5.110
98.795
                                                                                                                      Homo sapiens
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                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409
                     VERSION
KEYWORDS
                                                                                                                                                                                                                           REFERENCE
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ORIGIN

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MGI:647862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
ORIGIN
                  ORGANISM
                                                                                                                                     TITLE
JOURNAL
COMMENT
                                                         REFERENCE
                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208
                                                                                                                                                                                                                                                                                                                               FEATURES
     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="ATCC (inhost):110668"
/db_xref="taxon:9606"
/clone_lib="Colon carcinoma (HCC) cell line II"
/csole_Ltype="colon"
/cell_Ltype="KM12C"
/cell_line="KM12C"(HCC)-parental human colon carcinoma ;Dukes B2"
/note="Organ: colon; Vector: pBluescript SK-; Site_I:
EcoRI; Site_2: XhoI"
109 c 101 g 136 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eValThrGluTyrMetProAsnGlySerLeuAsnGluLeuLeuHisArgL 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             143 uHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsnGluPheHisV 160
                                                                                                                                                                                                                                                                                                                                                                                   102 GAAAGGATGTCTTAAGAGAAGCTGAAATTTTACACAAAAGCTAGATTTAGT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 alLysIleAlaAspPheGlyLeuSerLysTrpArgMetMetSerLeuSer 176
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                                                                                                                                                                                                                                                                                                              TyrIlePheProIleLeuGlyIleCysAsnGluProGluPheLeuGlyIl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             152 TACATTCTTCCAATTTTGGGAATTTGCAATGAGCCTGAATTTTTGGGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                          rgLysAspValLeuArgGluAlaGluIleLeuHisLysAlaArgPheSer
                                                                                                                                                                                                       Gaps: 1
Percent Identity: 98.137
                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                      from: 1 to: 484
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                                                                                                                                                                                        820.00
5.157
98.758
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US-09-445-223-1 x AA315575
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Percent Similarity:
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                                                                                                                       BASE COUNT
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VERSION
KEYWORDS
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The Wash U-HHMI Mouse EST Project
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/lab_host="SOLR (kanamycin resistant)"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 503)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1996)
Contact: Marra MyMouse EST Project
WashD-HHMI Mouse EST Project
WashD-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1810
Fax: 314 286 1810
Fax: mousesetstewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="NIH/Swiss"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 eHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMetMetSerL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 TCATGTTAAGATTGCAGATTTTGGTTTATCAAAATGGCGCATGATGTCAC 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CTGCTTCATCATCATAAAGACTAAAAGACTCAGAATATCTTGTTGGATAATGAATT
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Percent Identity: 91.617
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/organism="Mus musculus"
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Location/Qualifiers
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US-09-445-223-1 x AA655189
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alignment_scores
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1. 510
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Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC2&t2=RC2-ST0173-041099-011-e06&t3-1999-101-0.04&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 13
High quality sequence storp: 510.
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RC2-ST0173-041099-011-e06 ST0173 Homo sapiens CDNA, mRNA sequence.
AW389863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                   258
                                                                                                                                                                                                                                                                                                               258 pileProHisArgAlaArgMetIleSerLeuIleGluSerGlyTrpAlaG 275
                                                                                                                                                                                                                                                                      401
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                                                                                                                                                                                                                                                                                                                                                                                                         292 ProValLeuArgThrPheGluGluIleThrPheLeuGluAlaValIleGl
202 GAAGCATGATATACAGCTATGCAGTTATCATGTGGGAAGTGTTATCCA
                                                                                                                                     242 ValSerGlnGlyHisArgProValIleAsnGluGluSerLeuProTyrAs
                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vert
Mammalia; Eutheria; Primates; Catarrhini; Hc
1 (bases 1 to 510)
HCGP http://www.ludwig.org.br/ORESTES.
The FAPESP/LICR Human Cancer Genome Project
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Simpson A.J.G.
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LOCUS AW389863
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BASE COUNT ORIGIN

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168 rLysTrpArgMetMetSerLeuSerGlnSerArgSerSerLysSerAlaP 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 roGluGlyGlyThrIleIleTyrMetProProGluAsnTyrGluProGly 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 CCATTGAGATTTCGCATCCTGAATGAAATTGCCATTGGTGAAATTACCT 314
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                                                                                                                                                                                               460
                                                                                                                                                                                                                                                                                                                                113 CAAAAATCCAGGGCCAGTATCAAGCACGATATATATAGCTATGCAGTTAT 64
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                                                                                                                                                                                                                                                                                                            52 isThrProLeuLeuAspSerGluArgLysAspValLeuArgGluAlaGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102 erLeuAsnGluLeuLeuHisArgLysThrGluTyrProAspValAlaTrp
                                                                                                                                                               19 AlaAspLeuArgTyrLeuSerArgGlyAlaSerGlyThrValSerSerAl
                                                                                                                                                                                                                                                                                                                                                                                69 IleLeuHisLysAlaArgPheSerTyrIlePheProIleLeuGlyIleCy
                                                                                                                           to: 510
                 Gaps: 2
Percent Identity: 72.851
                                                                                                                         Align seg 1/1 to reverse of: AW389863 from: 1
                                                                                       US-09-445-223-1 x AW389863/rev
798.50
4.810
75.113
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     Quality:
                                    Percent Similarity:
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Percent Identity: 99.630
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Windows 95
SOFTWARE: FASTSEQ for Windows Version 2.0b
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Berlin, John
TITLE OF INVENTION: DOMAIN POLYPEPTIDES
TATLE OF INVENTION: DOMAIN POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/019,942
FILING DATE: 06-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTOREX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35,283
REGISTRATION NUMBER: 35,283
REFERENCE/POCKET NUMBER: 07334/06
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-6970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09019942
Patent No. 6033855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-445-223-1 x US-09-019-942-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1931 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.226
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
COUNTRY: USA
ZIP: 02110-2804
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Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
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2.3e-20 2
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3.5e-24
9.6e-24
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5.3e-22
5.3e-22
5.3e-22
5.3e-22
5.3e-22
1.1e-21
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                                                                                                                                      About: Results were produced by the GenCore software, version Copyright (c) 1993-2000 Compugen Ltd.
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/ptodata/1/ina/6B_COMB.seq:US-09-221-928-4
/ptodata/1/ina/6B_COMB.seq:US-09-221-527-4
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Database sequences: 302631
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Search time (sec): 68.920000
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                                                                   Date: Jun 13,
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 67
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                                                                                                                                                               leCysAsnGluProGluPheLeuGlyIleValThrGluTyrMetProAsn
                                                                                      GlySerLeuAsnGluLeuLeuHisArgLysThrGluTyrProAspValAl
                                                                                                                                                                                                                                                                                                                               764 CACCAGAAGGAGGACAATTATCTATATGCCACCTGAAAACTATGAACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skin Cells
pLeuIleMetLysGluAspTyrGluLeuValSerThrLysProThrArgT
                                                                                                                                                                                                                                                                                                                                                                                                                           hrSerLysValArgGlnLeuLeuAspThrThrAspIleGlnGlyGluGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PheAlaLysValIleValGlnLysLeuLysAspAsnLysGlnMetGlyLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    uGlnProTyrProGluIleLeuValValSerArgSerProSerLeuAsnL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MetThrGluAlaCysLeuAsnGlnSerLeuAspAlaLeuLeuSerArgAs
                                                         oGlnAspAsnAspPheLeuSerArgLysAlaGlnAspCysTyrPheMetL
                                                                                                                  ysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrIleSerGly
                                                                                                                                                                         SerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerAl
                                                                                                                                                                                                                                                                                                                                                                 Sequence 257, Application US/09188930A
Fatent No. 6150502
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From SK1;
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 257
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us-09-445-223-1.p2n.rni

			26 92	43	56 180	73	90	106 324	123 362	140	156 462	173 512	188 550	204 594	220	237	253 732	267
t_scores: 579.00 Length: 540 Quality: 579.00 Gaps: 26 Similarity: 54.444 Percent Identity: 34.074	t_block: 45-223-1 x US-09-188-930-257	eg 1/1 to: US-09-188-930-257 from: 1 to: 3516	LeuProThrIleProTyrHisLysLeuAlaAspLeuArgTyrLeuSerAr 	gGlyalaSerGlyThrValSerSerAlaargHisAlaaspTrpargValG ::: ::::: ::: :::: GGGGGGTTCGGGCAGGTGTACAAGGTGCGCATGTGCAAGAAGGT	<pre>lnValAlaValLysHisLeuHisIleHisThrProLeuLeu ::: :: GCCTCGCGATCAAGTGCTCGCCCAGTCTGCACGTCGAC</pre>	AspSerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLysAl	aargPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGluP ::: :: ::	heLeuGlylleValThrGluTyrMetProAsnGlySerLeuAsnGluLeu :::	LeuHisargLysThrGluTyrProAspValAlaTrpProLeuArgPheAr	glleLeuHisGlulleAlaLeuGlyValAsnTyrLeuHisAsnMetThrP :::	roProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspAsn 	GluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMetMe::::::	tSerLeuSerGlnSerArgSerSerLysSerAlaProGluGlyG	lyThrIleIleTyrMetProProGluAsnTyrGluProGlyGlnLysSer :::	ArgalaSerIlelysHisAspIleTyrSerTyrAlaValIleThrTr.	pGluValLeuSerargLysGlnProPheGluAspValThrAsnProLeuG :::	InileMetTyrSerValSerGlnGlyHisArgProValileAsnGluGlu::	SerLeuproTyrAspileProHisArgAlaArgMetileSe
alignmen	alignment_bl US-09-445-2	Align s	10	26 93	43	57	73	90	107 325	123 363	140	157	173	188 551	205	220	237	254 733

267	/TrpAlaGlnAsnProAspGluArgProSerP TIGGCATGCACACAGGGGGCCC
00	sCysLeuIleGluLeuGluProValLeuArgThrPheGluGluIle 30
826	
0	rPheLeuGluAlaValileGlnLeuLysLysThrLysLeuGlnSerVa 31.
841	
317	/sLysMe ?TGATGA
334	IleProValAsnHisGlyProGlnGluGluSerCysGlySerSe
888	GACCTGGCTCATGAGCGCGAGAAAAGCTCTCTAGAGTCCAAG 933
351	LeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPr 367 :: :: :: : AGTGAGGCCAGGCCGGAGTCCTCAGGCTCAAGGGGCTTGAAGGGCGCTTGAAGGGCTTGAAGGGCTTGAAGGGCTTGAAGGGCTTGAAGGGCTTGAAGGGCTTGAAGGGCTTGAAGGGCTTGAAGGGGCTTGAAGGGGCTTGAAGGG
	t 38
984	
384	LysLeuHisHisCysProGlyAsnHisSerTrpAspSerThrileSerGl 400
1016	TITITITITITITITITITITITITITITITITITITI
1036	10 ySerGlnArgAlaAlaPheCysAspHisLysThrThrProCysSerSerA 417
4	0 43
	TCCA 11
434	94 Glyllealagln
444	gGluAspIleValAsnGlnMetThrGluAlaCysLeuAsnGlnSerLeuA 461
1156	
461	λ
1173	ACTGTCTTTTGAGC1186
478	SerThrLysProThrArgThrSerLysValArgGlnLeuLeuAspThr 493
1187	
494	ThrAspIleGlnGlyGluGluPheAlaLysValIleValGlnLysLeuLy 510
1216	ACAGACATCCAGAAGAAGAAGCTAGTGGGATGCCATCATATCAGGGGACAC 1265
510	SASPASnLysGlnMetGlyLeuGlnProTyrProGluIleLeuValValS 527
1266	'ATGAAGATCCTACAGCCCCAAGATGTGGACTTGGTTCT
527	erArgSerProSerLeu 532 :: A ACAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
Ē	. /canl 7/ntodata/1/in
j :	
sed_docur	_documentation_block: equence 66, Application US/09188930A

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APPLICANT: Onrust, Rene
APPLICANT: Onrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REPERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEC ID NOS: 348
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 66
LENGTH: 1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 gileLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetThrP 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 LeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPheAr 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 gGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTrpArgValG 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 AspSerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLysAl 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LeuProThrIleProTyrHisLysLeuAlaAspLeuArgTyrLeuSerAr 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43 CTGCGCACCTTCGACGCCGGCGAATTCGCAGGCTGGGAAGGTGGGCTC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 541
Gaps: 27
Percent Identity: 33.272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from: 1 to: 1888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: US-09-188-930-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-445-223-1 x US-09-188-930-66
                                                                                                                                                                                                                                                                                                                                    ; LOCATION: (1690)...(1690)
; NAME/KEY: unsure
; LOCATION: (1755)...(1755)
; NAME/KEY: unsure
; LOCATION: (1864)...(1864)
US-09-188-930-66
                                  APPLICANT: Strachan, Lorna APPLICANT: Sleeman, Matthew
GENERAL INFORMATION:
APPLICANT: Watson, James D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548.00
1.845
54.898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
   Quality:
    Ratio:
   Percent Similarity:
                                                                                                                                                                                                                                                                                  ORGANISM: mouse
                                                                                                                                                                                                                                                                 TYPE: DNA
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157	GluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMe 172 ::::::::::::::::::::::::::::::::::::	
72	twetSerLeuSerGlnSerArgSerSerLysSerAlaProGluGly 187	
188 551	GlyThrIleIleTleTyrMetProProGluAsnTyrGluProGlyGlnLys 203	
204	SerargalaSerIleLysHisAspIleTyrSerTyralaValileTh 219	
219	rTrpGluValLeuSerArgLysGlnProPheGluAspValThrAsnProL 236	
236	euGlnIleMetTyrSerValSerGlnGlyHisArgProValIleAsnGlu 252	
253	GluSerLeuProTyrAspIleProHisArgAlaArgMetIl 266	
266	eSerLeuileGluSerGlyTrpAlaGlnAsnProAspGluArgFroSerP 283	
283	heLeuLysCysLeuIleGluLeuGluProValLeuArgThrPheGluGlu 299	
0 ,	IleThrPheLeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSe 316	
4 T		
33	uAsnileProvalAsnHisGlyProGlnGluGluSerCysGlySerSer 34	
0 4	GINLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAl 366 ::: ::: :::	
366 984	32	~ 6
383	99	æ
399 1039	16	73 52
416 1074	32	2 8
433	ProGlylleAlaGlnGlnTrplleGlnSerLy 443	8 10

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The control of the co	•
ThrThrAspileGlnGlyGluGluPheAlaLysValIleValGlnLysLe	
ulysaspasniysGlnMetGlyLeuGlnProTyrProGluIleLeuValV :::::::::::::::::::::::::::::::::::	,
name: docume equence equence equence equence APPLI	,
tation_block: 14, Application US/08444005 156/474 ANT: Leder, Philip ANT: Stenger, Ben Z. ANT: Lee, Tae-Ho ANT: Kim, Emily ANT: Kim, Emily OF SEQUENCES: 35 PONDENCES: 35 CONSECTE AND RESIST AND	
INFORMATION: ANT: Leder, Philip ANT: Seed, Brian ANT: Stanger, Ben 2. ANT: Ete, Tae-Ho ANT: Kim, Emily OF INVENTION: CELL DEATH PROTEI OF INVENTION: A Richardson P.C. EET: 225 Franklin Street, Suite EE: MA THY: USA	
n 2. LL DEATH PROTEI 5 chardson P.C. Street, Suite	
Street, Suite	
E: Fish & Richardson P.C. 225 Franklin Street, Suite AA AAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAA	
STATE: MA STONERY: USA	
1000 00100	
LIF: 02110-2804 COMPUTER READABLE FORM: MEDITIM MYDE: Diamon 3:ab	r
AT	
APPLICATION NUMBER: US/08/444,005 FILING DATE: 435 CLASSIFICATION: 435	
ATTORNEY/AGENT INFORMATION: NAME: Clark, Paul T.	
REGISTRATION NUMBER: 30,164 REFERENCE/DOCKET NUMBER: 00383/026001	
TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070 TELEPHONE: 617/542-5070	
TELEX: 200154 INFORMATION FOR SEQ ID NO: 14:	
SEQUENCE CHARACTERISTICS: LENGTH: 2268 base_pairs	
NES	
MOLECULE TYPE: DNA 5-08-444-005-14	
Quality: 397.00 Length: 609	_

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309 GAACTATTCGCTGGTGATGGAGTACATGGAGAGGGCAACCTGATGCACG 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 ArgileLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetTh 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 snGluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMet 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 alSerGlnGlyHisArgProValIleAsnGlu.....GluSerLeuPro 256
                                                                                                                                                                                                                                                                                      168 TGGATTTGTCATCCTGAAAAA......GTATACACAGGGCCCAACC 208
                                                                                                                                                                                                                                                                                                                                                         209 GCGCTGAGTACAATGAGGTTCTCTTGGAAGAGGGGGAAGATGATGCACAGA 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 uPheLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluL 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 MetSer...LeuSerGlnSerArgSerSerLysSerAlaPro..... 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ||| :::||| || 644 ACCTGAATGACATCAAAGCCCACGGAGAAAGTCG...... 681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 LysHisAspileTyrSerTyrAlaValileThrTrpGluValLeuSerAr 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 gLysGlnProPheGluAspValThrAsnProLeuGlnIleMetTyrSerV 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 825
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                                                                                                                                                                                              106 euLeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPhe 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              257 TyrAspIleProHisArgAlaArgMetIleSerLeuIleGluSerGlyTr 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           273 pAlaGlnAsnProAspGluArgProSerPheLeuLysCysLeuIleGluL 290
                                                                                                                                                               40
                                                                                                                                                                                                                                                                                                                                                                                                                 73 AlaArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGl 89
                                                                                                                                                                                                                                             40 pArgValGlnValAlaValLySHisLeuHisIleHisThrProLeuLeuA 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24 LeuSerArgGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTr
                                                                                                                                                                                                                                                                                                                               57 spSerGluArgLysAspVal...LeuArgGluAlaGluIleLeuHisLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ::||| ||||||::
359 TGCTA.....AAGACCCAGATA...GATGTCCCACTTTCATTGAAAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                826 AGGGAGATC.....ATCAGCCTCATGGAGCGTGCTG
Gaps: 25
Percent Identity: 25.452
                                                                                                                      from: 1 to: 2268
                                                                                                                      lign seg 1/1 to: US-08-444-005-14
                                                          lgnment_block:
3-09-445-223-1 x US-08-444-005-14
Ratio: 1.272
ercent Similarity: 51.232
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955

361

1155

341

325

443

485

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.740 CACCACTAGTCTGACTGATGAACACCTGAACCCTATCAGGGAAAACCTGG 1789
                                                                                                  1790 GAAGGCAGTGGAAAAACTGTGCCCGCAAGCTGGGCTTCACTGAGTCTCAG 1839
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    139 hrProProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAsp 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ....LeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGlu 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 CCAAGCCGCTCTGGTGACTAAATTCATGGAGAACGCCTCCTTGTCGGGG 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 crecrecaercccaereccryeccc.....resccecrcrrrs 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 eArgIleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetT 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LysAspValLeuArgGluAlaGluIleLeuHisLysAlaArgPheSerTy 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 alAlaValLySHisLeuHisIleHisThrProLeuLeuAspSerGluArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCCTTGGTGTCCATCGAGGAACTGGAGAACCAGGAGCTCGTCGGCAAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 ProThrIleProTyrHisLysLeuAlaAspLeuArgTyrLeuSerArgGl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rIlePheProIleLeuGlyIleCysAsnGluProGluPhe......
                                                     ....GluPheAlaLysValIleValGl
                                                                                                                                                                                                                                                      seq_name: /cgn1_7/ptodata/1/ina/6A_COMB.seq:US-09-329-418-2
                                                                                                                                                                                                                                                                                           seq_documentation_block:
    Sequence 2, Application US/09329418
    Sequence 2, Application US/09329418
    Sequence 2, Application US/09329418
    GENERAL INFORMATION:
    APPLICANT: ENECA Limited
    TITLE OF INVENTION: PROTEIN ACTIVATOR OF APOPTOSIS
    TITLE PEFERENCE: PHM.70536
    CURRENT APPLICATION NUMBER: US/09/329,418
    CURRENT FILING DATE: 1999-06-11
    NUMBER OF SEQ ID NOS: 39
    SOFTWARE: FastSEQ for Windows Version 3.0
    SEQ ID NO 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 499
Gaps: 21
Percent Identity: 28.056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1 to: 1557
                                                                                                                                                                                                         1840 ATCGATGAATCGACCATGACTATG 1864
                                                                                                                                                       nLysLeuLysAspAsnLysGlnMet 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1 to: US-09-329-418-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-445-223-1 x US-09-329-418-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 TGGCGGTCAAGATCGTAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      395.00
1.452
54.509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
CORGANISM: Homo Sapiens
US-09-329-418-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1557
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1253 GTCCTGGACCCCGAGGGAATCAGGGGGCC	409 isLysThrThrProCysSerSerAlaIleIleAsnPro 		205 591 ·	222 641 .	239	254 732	268	UL 285 CRGANISM: Homo Sapiens US-09-329-418-1 GG 832	Thr 301 alignment_scores: Ouality: 392.50 Length Ratio: 1.443 Gaps AAC 876 Percent Similarity: 54.291 Percent Identity	alignment_block: US-09-445-223-1 x US-09-329-418-1 926	330 Alig 976	338 204 1026 27	350 254 1076 44	367 55 1102 61	377 77 77 1152	379 377 1202 87	Hi 392 Hi 392 104 AsnGluLeuLeuHisArgLysThrGluTyFPPOASpVa	474
### ##################################	156 AsnGluPheHisValLysIlealaAspPheGlyLeuSerLysTrpArgMe	tMetSerLeuSerGlnSerArgSer ::: ::	189 hrileileTyiMetProProGludsnTyrGluProGlyGlnLysSerArg	206 AlaserIleLysHisAspIleTyrSerTyrAlaValIleThrTrpGluVa 	222 lLeuSerargLysGlnProPheGluAspValThrAsnProLeuGlnIleM	239 etTyrSerValSerGlnGlyHisArgProValIleAsnGluGluSer::	255 LeuProTyrAspileProHisArgAlaArgMetIleSerLe	268 uIleGluSerGlyTrpAlaGlnAsnProAspGluArgProSerPheLeuL 	285 ysCysLeuIleGluLeuGluProValLeuArgThrPheGluGluIleThr::: ::: ::: - ::: ::: 833 AATGCTACCAAAAACTGATGAGTCTTCCAGATGGTGGAGAAC	302 PheLeuGluAlaValIleGlnLeuLysLysThrLysLeuGlnSerValSe :::::: ::::::: :::::::::::	318 rSer.AlaileHisLeuCysAspLysLysLysMetGlu	331LeuSerLeuAsnIleProvalAs ::::: ::: 977 AAATGGATGGCTTTAGGAGAACCATAGAAAACCAGCACTCTCGTAATGAT		351 LeuHisGluAsnSerGlySerProGluThrSerArgSerLeuProAlaPr 	367 oGlnaspasnaspPheLeuSerargLysala	378Glnasp ::: :::	380 CysTyrPheMetLysLeuHisHisCysProGlyAsnHi 110	

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....... 1286
                                                           InTrpileGlnSe 442
||| || || || || CTGGGGTGCAAG 1378
                                   GGAGCCAAATCC 1328
                                                                                                                                                                                                                                                                                                                                                                                                                                               YrLeuserArgGl 27
:::::::|
:TCGTCGCAAAGG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oTrpArgValGlnV 44
||||
|TGGGGCTACGATG 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCTCGAGCCAAG 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alAlaTrpProLe 120
|||||||||
.....TGGCCGCT 514
                     LeuSerThrAla 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....TCG 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGATAACGAATT 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 uArgPheArgIleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisA 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AspSerGluArg 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      aArgPheSerTy 77
                                                                                                                                          09-329-418-1
                                                                                                  CysLeu 456
|||||||
|TGCCTT 1421
                                                                                                                                                                                                                                                                                                                                                         h: 501
s: 22
y: 28.144
                                                                                                                                                                                                                                                                                                                                                                                                                             :0: 1873
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1364 AGAGACCTCAACTTTCAGAAACCAGATGCCCAGCCCTACCTCAACTGGAA 1413

390	00
1363	377
1313	₹
77	365 oAlaProGlnAspAsnAspPheLeuSerArgLysAla
365 1263	349 SerGlnLeuHisGluAsnSerGlySerProGluThrSerArgSerLeuPr
348 1237	337 .Valasn.HisGlyproClnGluGluSerCysGlySer :::
336 1187	331LeuSerLeuAsnIlePro
330 1137	316 rValSerSer.AlaileHisLeuCysAspLysLysMetGlu .::: 1088 GCTCAGGAGCAGCAATAGGAGATTTCTATCCCAGAGTCAGGCCAAGGAG
316 1087	300 IleThrPheLeuGluAlaVallleGlnLeuLysLysThrLysLeuGlnSe :: ::::: :::::
299 1040	283 heLeuLysCysLeulleGluLeuGlubroValLeuArgThrPheGluGlu ::: ::: :: :::: 994 TCCAGGAATGCTACCAAAAACTGATGATGATGATGGTGGTGGG
283 993	266 eSerLeulleGluSerGlyTrpalaGlnAsnProAspGluArgProSerP ::: :::::
266 943	253 GluSerLeuProTyrAspileProHisArgAlaArgMetil CTGCCCCAAGCCGGCCTGAGACTCCCGGCTTAGAAGGACTGAA
252 899	237 lnileMetTyrSerValSerGlnGlyHisArgProVallleAsnGlu ::: :: ::: :::
237 849	220 pGluValLeuSerArgLysGlnProPheGluAspValThrAsnProLeuG :
220 802	204 SerargalaserileLysHisAspileTyrSerTyrAlaValileThrf: ::::
203 752	187 lyGlyThrIdelleTyrMetProProGludsnTyrGluProGlyGlnLys (
187 705 ·	170 pargmetMetSerLeuSerGlnSerArgSerSerLysSerAlaProGluG 3 ::: ::: :::
170 664	154 LeuaspasnGluPheHisValLysIleAlaAspPheGlyLeuSerLysTr 1 ::
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564	

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1490 AAATCCAGTAACAGGGCGACCGCTCGTTAACATATACAACTGCTCTGGGG 1539
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APPLICANT: Ecker, Joseph R.
APPLICANT: Kieber, Joseph B.
TITLE OF INVENTION: Constitutive Triple Response Gene and
TITLE OF INVENTION: Mutations
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Woodcock, Washburn, Kurtz, Mackiewicz and
ADDRESSE: No. 5377065ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                             407 ysAspHisLysThrThrProCysSerSerAlallelleAsnProLeuSer 423
                                                                                                                                                            424 ThralaGlyAsnSerGluArgLeuGlnProGlyIleAlaGlnGlnTrpIl 440
                                                                                                                                                                                                                                                                 390 yAsnHisSerTrpAspSerThrIleSerGlySerGlnArgAlaAlaPheC 407
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                                        1414 CACCAAGTCCTGGACCCCGAGGGAATCAGGGGGCTGAGAG......
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Gaps: 12
Percent Identity: 30.721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/928,464 FILING DATE: 19920810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           томыек: US/07/928,464
19920810
N. . .
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ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: UPN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568 3100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2890 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
    Sequence 1, Application US/07928464
    Patent No. 5367065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32,279
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US-09-445-223-1 x US-07-928-464-1
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ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzanne E.
REGISTRATION NUMBER: 32,
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1.861
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: NUCLEIC
STRANDEDNESS:
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; LOCATION:
US-07-928-464-1
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STATE: PA
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                                                                                                                                                                                                                                                                         1766 ATCTTAATATAAAAGAAAGATTGGAGCAGGTTCCTTTGGCACTGTCCAC 1815
                                                                                                                                                                                                                                                                                                                                                 1675 ATGAATGCCCCACCAATCAGTCAGCCAGTTCCAAACAGGGCAAATAGGGA 1724
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 ..ArgAlaArgMetIleSerLeuIleGluSerGlyTrpAlaGlnAsnPro 277
                                                                                                                                                                                                                                                                                                                         49
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                                                                                                                                                                                                                                                                                                                                                                                                          50 .HisIleHisThrProLeuLeuAspSerGluArg...LysAspValLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213 yrSerTyrAlaValIleThrTrpGluValLeuSerArgLysGlnProPhe
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                                                                                                                                        13 ......lleProTyrHisLysLeuAlaA
                                                                                                                                                                                                                                                                                                                    37 HisAlaAspTrpArg...ValGlnValAlaValLysHisLeu.....
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  to: 2890
Align seg 1/1 to: US-07-928-464-1 from: 1
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    Sequence 1, Application PC/TUS9307347
    GENERAL INFORMATION:
    APPLICANT: Ecker, Joseph R.
    APPLICANT: Ecker, Joseph R.
    TITLE OF INVENTION: Constitutive Triple Response Gene and TITLE OF INVENTION: Mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1675 ATGAATGCCCCACCAATCAGTCAGCCAGTTCCAAACAGGGCAAATAGGGA 1724
278 AspGluArgProSerPheLeuLysCysLeuIleGluLeuGluProValLe 294
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                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz and
ADDRESSEE: Norris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 319
Gaps: 12
Percent Identity: 30.721
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CITY: Philadelphia
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ATTORNEY/AGENT INFORMATION:
NAME: Miller, Suzane E.
REGISTRATION NUMBER: 32,279
REFERENCE/DOCKET NUMBER: UPN-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2890 base pairs
TENGTH: 2890 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS.
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1.861
63.323
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CORRESPONDENCE ADDRESS:
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                                                                                                                               2544 CAAATCA 2550
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Percent Similarity:
                                                                                       294 uArgThr 296
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 19103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: PA
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; LOCATION:
PCT-US93-07347-1
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seq_documentation_block:

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2371 GGTAACTTA...AATCCGGCTCAGGTTGTAGCTGCGGTTGGTTTCAAGTG 2417
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                                                                                                                                                                                                                                    .........GCTGAGCGTGTTAATGAGTTCTTAA 1900
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                                             1766 ATCTTAATATAAAAGAAAAGATTGGAGCAGGTTCCTTTGGCACTGTCCAC 1815
                                                                                                                                 :::[||:::|||:::|
1816 CGTGCTGGGATGGCTCGGATGTTGTGAAATTCTCATGGAGCA 1865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 heGlyLeuSerLysTrpArgMetMetSerLeuSerGlnSerArgSerSer 181
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20. spLeuArgTyrLeuSerArgGlyAlaSerGlyThrValSerSerAlaArg 36
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                                                                                                  37 HisAlaAspTrpArg...ValGlnValAlaValLySHisLeu.
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                                      GENERAL INFORMATION:
APPLICANT: ECKer, Joseph R.
APPLICANT: ECker, Joseph R.
APPLICANT: Ecker, Joseph J.
TITLE OF INVENTION: CONSTITUTION TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: WOOGCOCK Washburn Kurtz Mackiewicz and
ADDRESSEE: No. 544166ris
STREET: One Liberty Place - 46th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 319
Gaps: 12
Percent Identity: 30.721
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                                                                                                                                                                                                                                                                                                                                                                                                        January 12, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/928,464
Sequence 1, Application US/08003311B; Patent No. 5444166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: August 10, 1992
ATGNEY AGENT INFORMATION:
NAME: LOTI Y. Beardell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: US-08-003-311B-1
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US-09-445-223-1 x US-08-003-311B-1
                                                                                                                                                                                                                                                                                                                                                             IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION NUMBER: US/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3033 base pairs
                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IBM PC COMPA
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1.861
63.323
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STRANDEDNESS: single
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118..2583
                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
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MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                 STATE: PA
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COCATION:
US-08-003-311B-1
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APPLICANT: Ecker, Joseph R.

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                                                                                                                                                                                                                                                                                                                                                         98 tProAsnGlySerLeuAsnGluLeuLeuHisArgLysThrGluTyrProA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148 sThrGlnAsnIleLeuLeuAspAsnGluPheHisValLysIleAlaAspP 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 heGlyLeuSerLysTrpArgMetMetSerLeuSerGlnSerArgSerSer 181
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                                                                   50 .HisIleHisThrProLeuLeuAspSerGluArg...LysAspValLeuA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 rgGluAlaGluIleLeuHisLysAlaArgPheSerTyrIlePheProIle
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                                                                                                                                                                                                                                                                82 LeuGlyIleCysAsnGluProGluPheLeuGlyIleValThrGluTyrMe
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Patent No. 5602322
GENERAL INFORMATION:
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37 HisalaaspTrparg...valGlnValalaValLySHisLeu....... 49
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1815 CGTGCTGAGTGGCTCGGATGTTGCTGTGAAATTCTCATGGAGCA 1865
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APPLICANT: Kieber, Joseph J.
TITLE OF INVENTION: Constitutive Triple Response Gene
TITLE OF INVENTION: and Mutations
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
ADDRESSEE: Woo 5603322ris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MetAsnGlyGluAlaIleCysSerAlaLeuProThr........
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Gaps: 12
Percent Identity: 30.721
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                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Worderfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/261,432
FILING DATE: June 17, 1994
CLASSIFICATION NUMBER: US/08/261,432
FILING DATE: June 17, 1994
PRIOR PAPLICATION DATE: 1993
ATTORNEY AGENT INFORMATION:
NAME: LOTI Y. Beardell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: UPN-1864
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 303 Base Pairs
                                                                                                                                                                                                                                                               ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-445-223-1 x US-08-261-432-1
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1.861
63.323
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                                                                                                                                                                                                                                                    U.S.A.
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Ratio:
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                                                                                                                                                                                                 CITY: Phil
STATE: PA
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                                                                                                                                                                                                                                                  COUNTRY:
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2051 AATTAGATGAGAGGCGCGCCCGAGTATGCCTTATGATGAGGGA 2100
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2286 GCGAGAIGAGCCGTCTAAIGAA......AAGTCAGAIGIGI 2320
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| ACAGCTICGGGGTCATGTGGGAGCTTGCTACATTGCAACAACAACGATGG 2370
......GCTGAGCGTGTTAATGAGTTCTTAA 1900
                                                                                                                   1901 GAGAGGTTGCGATAATGAAACGCCTTCGCCACCCTAACATTGTTCTCTTC 1950
                                                                                                                                                                                                             2201 TIGGICICICGCGATIGAAGGCCAGCACGTITCTITCCICGAAGICAGCA 2250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heGlyLeuSerLysTrpArgMetMetSerLeuSerGlnSerArgSerSer 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                yrSerTyrAlaValIleThrTrpGluValLeuSerArgLysGlnProPhe 229
                                                                                                                                                                                                                                                                                                 98 tProAsnGlySerLeuAsnGluLeuLeuHisArgLysThrGluTyrProA 115
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APPLICANT: HSU, HAILING
APPLICANT: GOEDBEL, DAVID V
TITLE OF INVENTION: RIP: NOVEL HUMAN PROTEIN INVOLVED IN
                                                                                                                                                                                                                                                                                                                                   rgGluAlaGluIleLeuHisLysAlaArgPheSerTyrIlePheProIle
                                                                                                                                                                              82 LeuGlylleCysAsnGluProGluPheLeuGlylleValThrGluTyrMe
                                                                                                                                                                                                                                                                                                                                                                                                                    115 spValAlaTrpProLeuArgPheArgIleLeuHisGluIleAlaLeuGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197 .AsnTyrGluProGlyGlnLysSerArgAlaSerIleLysHisAspIleT
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Patent No. 621137
GENERAL INFORMATION:
APPLICANT: BAICHWAL, VIJAY R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block
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1866 AGACTTCCAT...
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TUMOR NECROSIS FACTOR SIGNAL TRANSDUCTION, AND SCREENING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89 uPheLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluL 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           208 CTGAGACACAGCCGGGTGAAGCTCCTGGGCGTCATAGAGGAAGG
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Gaps: 12
Percent Identity: 28.792
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-09-132-118-1 from: 1 to: 2016
                                                                                 E: SCIENCE & TECHNOLOGY LAW GROUP 75 DENISE DRIVE
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                                                                                                                                                                                                                             E: Floppy disk
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                              ATTORNET/AGENT INFORMATION:
NAME: OSMAN, RICHARD A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: T9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-445-223-1 x US-09-132-118-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPANE: (650) 343-4342
TELEPAN: (650) 343-4342
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2016 base pairs
                        ASSAYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.716
55.270
TITLE OF INVENTION: TUT
TITLE OF INVENTION: AS!
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369.00
                                                                                                                                                                                      ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC COM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
                                                                                                                           CITY: HILLSBOROUGH STATE: CALIFORNIA
                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
Percent Similarity:
                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucle;
STRANDEDNESS
                                                                                   ADDRESSEE:
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US-09-132-118-1
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                                                                                                                                                                    COUNTRY:
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957 GTCTCTTCAACTTGATTGTGTGGCAGTACCTTCAAGCCGGTCAAATTCAG 1006
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                                                                                                                                394 .AAAGGCGTGATACACAAGGACCTGAAGCCTGAAATATCCTTGTTGATA 442
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123 ArgileLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetTh 139
                                                                                                                                                                                                                                                                                                      173 MetSerLeuSerGlnSerArgSerSerLysSerAlaProGlu...... 186
                                                                                                                                                                                                                                                                                                                                                      493 TGGAGCAAACTGAATAATGAAGAGCACAATGAGCTGAGGGAAGTGGACGG 542
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725 AATCTGGGAACAGGCCAGATGTGGATGACATCACTGCCCAAGA 774
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                                                                                             139 rProProLeuLeuHisHisAspLeuLysThrGlnAsnIleLeuLeuAspA
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                             1124 AGAGTAAACTCCAAGAC 1140
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89 uPheLeuGlyIleValThrGluTyrMetProAsnGlySerLeuAsnGluL 106 158 GCATTGAGCACAACGAGGCCCTCTTGGAGGCGAAGATGATGATGAACAGA 207 109 .AGAACCCAGGGACTCATGATCATGAAACAGTGTACAAGGGGCCCCAACT 157 208 CTGAGACACAGCCGGGTGGTGAAGCTCCTGGGCGTCATCATAGAGGAAGG 257 56 euAspSerGluArgLysAspValLeuArgGluAlaGluIleLeuHisLys 72 24 LeuSerArgGlyAlaSerGlyThrValSerSerAlaArgHisAlaAspTr 40 40 pArgValGln...ValAlaValLySHisLeuHisIleHisThrProLeuL 56 73 AlaArgPheSerTyrIlePheProIleLeuGlyIleCysAsnGluProGl Length: 390 Gaps: 13 Percent Identity: 29.231 Align seg 1/1 to: US-08-444-005-16 from: 1 to: 2137 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: STATE: MA 00383/026001 APPLICANT: Stanger, Ben Z.
APPLICANT: Lee, Tae-Ho
APPLICANT: Kim, Emily
TITLE OF INVENTION: CELL DEATH PROTEIN
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS: APPLICATION NUMBER: US/08/444,005 Sequence 16, Application US/08444005 Patent No. 5674734 GENERAL INFORMATION: CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: CLark, Paul T. 80,164
REGISTRATION NUMBER: 30,164
REFERENCE/DOCKET NUMBER: 0038
TELECHOMUNICATION INFORMATION:
TELEPHONE: 617/542-670
TELEPHONE: 617/542-6906 INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 2137 base pairs TYPE: nucleic acid STRANDEDNESS: single alignment_block: US-09-445-223-1 x US-08-444-005-16 APPLICANT: Leder, Philip APPLICANT: Seed, Brian 369.00 1.732 54.615 ; MOLECULE TYPE: DNA US-08-444-005-16 RY: USA 02110-2804 Percent Similarity FILING DATE: alignment_scores: COUNTRY:

seq_name: /cgn1_7/ptodata/1/ina/5A_COMB.seq:US-08-444-005-16

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1057 ccrerecadedaccreerragerccracacacac......... 1095
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                                                       euLeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPhe 122
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                                                                                           308 TGCTGAAAGCCGAGATGAGTACTCCG.
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Sequence 1, APPLICATION US/09161443A
Sequence 1, APPLICATION US/09161443A
BAPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
APPLICANT: C. Frank Bennett
TITLE OF INVENTION: ANTISENSE MODULATION OF RIP-1 EXPRESSION
FILE REFERENCE: RTS-0011
CURRENT APPLICATION NUMBER: US/09/161,443A
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 uPheLeuGlyIleYalThrGluTyrMetProAsnGlySerLeuAsnGluL 106 ::::::||| | ||||||||| :::||| ::::
67 CTGGACAGCGGAGGCTTTGGGAAGGTGTCTCTGTGTTTCCAC..... 108
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                                                                                                                   seq_name: /cgn1_7/ptodata/1/ina/6A_COMB.seq:US-09-161-443-1
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Gaps: 12
Percent Identity: 28.792
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                                                                           1121 TGCAGAGTAAACTCCAAGAC 1140
                                         373 euSerArgLysAlaGlnAsp 379
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1.716
55.270
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo saplens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)..(2016)
                                                                                                                                                        seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 2311
OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: unsure
LOCATION: 2496
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       1096
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1124 AGAGTAAACTCCAAGAC 1140

374 erArgLysAlaGlnAsp 379

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1007 CCACAGAACAGCCTGGTTCACTGCACAGTTCCCAGGGACTTGGGATGGGT 1056
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258 GAAGTACTCCCTGGTGATGGAGTACATGGAGAAGGGCAACCTGATGCACG 307
                                                  euLeuHisArgLysThrGluTyrProAspValAlaTrpProLeuArgPhe 122
                                                                                                     ....CTTTCTGTAAAAGGA 348
                                                                                                                                                  123 ArgIleLeuHisGluIleAlaLeuGlyValAsnTyrLeuHisAsnMetTh 139
                                                                                                                                                                                  snGluPheHisValLysIleAlaAspPheGlyLeuSerLysTrpArgMet 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291 luProValLeuArgThrPheGluGluIleThrPheLeuGluAlaValIle 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    857 GGCCTTTTTATTTAAGTCAATTAGAAGAAAGTGTAGAAGAGGACGTGAAG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       907 AGTTTAAAGAAAGAGTATTCAAACGAAAATGCAGTTGTGAAGAGAATGCA 956
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     493 TGGAGCAAACTGAATAATGAAGAGCACAATGAGCTGAGGGAAGTGGACGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             543 CACCGCTAAGAAGAATGGCGGCACCCTCTACTACATGGCGCCCGAGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 MetSerLeuSerGlnSerArgSerSerLysSerAlaProGlu......
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                                                                                                  308 TGCTGAAAGCCGAGATGAGTACTCCG...
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229 heGluaspValThrAsnProLeuGlnIleMetTyrSerValSerGlnGly 245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 eTyrSerTyrAlaValIleThrTrpGluValLeuSerArgLysGlnProP 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51
seq_name: /cgn1_7/ptodata/1/ina/5A_COMB.seq:US-08-700-575-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GAAAACTATGAACCTGGACAAAAATCAAGGGCCAGTATCAAGCACGATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length: 69
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
COMPUTER: TEM PC COMPATIBLE
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to: 210
                                                                                                GENERAL INFORMATION:

APPLICANT: Au Young, Janice
APPLICANT: Hawkins, Olga
APPLICANT: Hawkins, Phillip R.
APPLICANT: Wilde, Craig G.
TITLE OF INVENTION: NOVEL HUMAN KINASE HOMOLOGS
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SP-100
                                                           Sequence 31, Application US/08700575
Patent No. 5817479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J
REGISTRATION NUMBER: 36749
REFERENCE/DOCKET NUMBER: SP-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-700-575-31
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US-09-445-223-1 x US-08-700-575-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31:
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                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 210 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality: 367.00
Ratio: 5.319
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                               CITY: PALO ALTO STATE: CA
                                         seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MELLIBRARY: THELLIBRARY: 156108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                           USA
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TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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seq_accumentation_block:

sequence 1, Application Us/08665625A

Patent No. 594301

GENERAL INFORMATION:

APPLICANT: UENO, Nacto
APPLICANT: WATSUMOTO, Kunihiro
APPLICANT: MATSUMOTO, Kunihiro
APPLICANT: MATSUMOTO, Kunihiro
APPLICANT: MATSUMOTO, Kunihiro
APPLICANT: MATSUMOTO, Kunihiro
APPLICANT: MIE, Kenji
ITILE OF INVENTION: TRANSDUCTION SYSTEM
NUMBER OF SEDUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREE: P.O. Box 1404
CORPUTER: United States
STRTE: Virginia
COUNTRY: United States
STRTE: Virginia
COUNTRY: United States
STRTE: Virginia
COUNTRY: United States
CONFUTER: EADABLE FORM:
COMPUTER: 18M PC compatible
OPPRATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/685,625A
FILING DATE: 29-SEP-1995
ATTORNEY/AGENT INFORMATION:
RESTSTRICATION NUMBER: JP 7-253549
FILING DATE: 29-SEP-1995
ATTORNEY/AGENT INFORMATION:
REFERENCE/DOCKET NUMBER: 36,607
TELECOMMUNICATION NUMBER: 36,607
102 TTGAAGATGTCACCAATCCTTTGCAGATAATGTATAGTGTGTCACAAGGA 151
                                                            13 IleProTyrHisLysLeuAlaAspLeuArgTyrLeuSerArgClyAlaSe 29
                                                                                                                                                                                                                                                                                                                      seq_name: /cgn1_7/ptodata/1/ina/5B_COMB.seq:US-08-685-625A-1
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Percent Identity: 25.127
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US-09-445-223-1 x US-08-685-625A-1
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        315.50
1.119
47.878
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; LOCATION: 157..1893
US-08-685-625A-1
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MOLECULE TYPE: CDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block
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Quality:
Ratio:
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                                                                                                                                                                                    262 galaarg 264
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1094	5 CCATTACAGTATCCTTGTCACTCTGATGAAGGGCAGAGCAACTCA	104
290	:	2
1044	83 hetelbyscysteuliedliledlileu	9 6
on i	GACACGCTGTTGGTCTAAGGACCCATCTCAGGGCCCTTCAATGGAGGAA	6
283	69 eGluSerGlyTrpAlaGlnAsnProAspGluArgProSer	7
944		9,
269	uSerLeuproTyrAspileProHisArgAlaArgMetileSerLeu	73
912	66 TCAGAATCATGTGGGCTGTTCATAATGGCACTGACCACCACTGATC	8
252	lleMetTyrSerValSerGlnGlyHisA	8
865	<pre>20 ps.tuvat_belaseragu_Scinkrovinestabagvatifikasirro 11 </pre>	7 8
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220 815	04 SerArgAlaSerIleLysHiaAspIleTyrSerTyrAlaVal1LeThrTr 	× ×
765	27GGAGTGCTGCTTGGATGCCGCCTGAAGTGTTTGAA	7.
203	7 lyGlyThrIleIleTyrMetProProGluAsnTyrGluProGlyGln	18.
726	99 CATCCAAACACACATGACCAATAATAAA	99
187	0	17
698	::: :: :: :: :: :: :: :: :: :: :: :: ::	9
170	5 AspAsnGluPheHisValLysIleAlaAspPheGlyLe	
154 648	39 NEPTOProLeuleuHishisaspheulysrnrGinashizeLeuleu 	
2	CAGTGTTCCCAAGGAGTGGCTTACCTGCACAGC	20
139	euHisGluIleA	11
561	ACTACACTGCTGCTCAT	Ŋ
122	2 GluTyrProAspValAlaTrpProLe	11
516	 AATATGCAGAGGGGGGGT	46
111	luTyrMetProAsnGlySerLeuAsnGluLeuLeuh	٠.
	1 GECAAGTIGIAGE GEGCCTGCCTGAATCCAGTATGTCTTGTG	4
95	8 ePheProIleLeuGlvIleCvsAsnGluProGluPheLeuGlvIl	
422	oz Aspvalleuargeluargellilesedelislysahaargeleszijiit 	, E
9	מייייייייייייייייייייייייייייייייייייי	
61	eHisThrProLe	7 8
337		55
2 2	JACTACRAGGAGAT CGAGGTGGAGAGAGATTGTCGGAAGAGGAGGT	, ``
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290		290
1095 CAC	CACCAGCACAGGCTCGTTCATGGACATTGCTTCTACAAATACCAGTAATA	1144
291		301
	PheLeuGluhlaVallleGlnLeuLysLysThrLysLeuGlnSerValSe	318
	TTGGAGTCAAAACTGTTGAAAAACCAGGCAAAGCAACAGAGTGAATC	0
318 rSe: :: 1245 rGG	rSerAlalleHisLeuCysAsplysLysMetGluLeuSerLeuAsnI :::	335 1294
335 leP	IPProValAsnHisGlyProGlnGluGluSerCysGlySerSerGlnLeu	351 1341
.352 His ::: 1342 GAA	HisGluasnSerGlySerProgluThrSerAr	362 1388
362 gSe 1389 ATC	9SerLeuProAlaProGlnAspAsnAspPheLeuSerArgLysAlaGlnA :: 	379 1404
379 SPC 1405 ACT	spCysTyrPheMetLysLeuHisHisCysProGlyAsnHisSerTrpAsp 	395 1418
396 Ser	CATCCAGCCC	402 1468
403	TCACTACCTCAGGACCAACGTCAGAGAPHECYSASP.H1sLySThr	411 1518
412 Thri 1519 ACC	ThrprocysSerSerAlallelleAsnproLe-	422 1568
422 uSe; ::: 1569 GGC	uSerThrAlaGlyAsnSerGluArgLeuGlnPro	433 1618
434 1619 ACT	Glyllealagingintrpileginserlysarg	444 1668
445 Glui 1669 GAG	GluaspileValasnGlnMetThrGlualaCysLeuAsnGl 	458 1718
458 nSe 1: 1719 AGA	nSerLeuAspAlaLeuLeuSerArgAspLeuIleMetLysGluAspTyrG :::	475 1759
475 luLe :: 1760 AA.	luLeuValSerThrLysProThrArgThrSerLysVal	487 1788
488 Arg(::: 1789 AAA	ArgGlnLeuLeuAsp 492 :::::: AAAAGCTTTTAGAT 1803	

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Access	DB#	

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _		E	xaminer # :	Date:
	Diama Nissanhan 20		Senal Number	
				PAPER DISK E-MAIL
f more than one search	is submitted, ple	ase prioritize	searches in order of ne	ed. *********
Please provide a detailed state	ment of the search topic structures, keywords, sy e any terms that may ha	, and describe as monyms, acronyn ve a special mean	specifically as possible the sub ns, and registry numbers, and c ning. Give examples or relevar	ject matter to be searched. ombine with the concept or
Title of Invention:				
Earliest Priority Filing D	Pate:			
*For Sequence Searches Only appropriate serial number.	Please include all pertin	ent information (po	arent, child, divisional, or issued p	patent numbers) along with the
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*************	******	of Search	**************************************	where applicable
STAFF USE ONLY	<i>u</i>	quence (#) 2	STN	
Searcher:	20	quence (#)	Dialog	
Searcher Location:	Structu	ıre (#)	Questel/Orbit	<u></u>
Date Searcher Picked Up:	J Biblio	graphic	Dr.Link	
Date Completed:	Litigat	tion	Lexis/Nexis	
Searcher Prep & Review Time:	Fullte:	xt	Sequence Systems	
Clerical Prep Time:		Family	www/Internet	
Online Time:	Other		Other (specify)	

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